

- Alignment No. 13362
  - gi No. 1542845
  - % Identity 83
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 1865: from 142 to 193
- Alignment No. 13363
  - gi No. 2315544
  - % Identity 79.2
  - Alignment Length 144
  - Location of Alignment in SEQ ID NO 1865: from 51 to 193
- Alignment No. 13364
  - gi No. 2996008
  - % Identity 80.4
  - Alignment Length 153
  - Location of Alignment in SEQ ID NO 1865: from 44 to 193
- Alignment No. 13365
  - gi No. 338687
  - % Identity 81.2
  - Alignment Length 149
  - Location of Alignment in SEQ ID NO 1865: from 46 to 193
- Alignment No. 13366
  - gi No. 3845214
  - % Identity 75.7
  - Alignment Length 144
  - Location of Alignment in SEQ ID NO 1865: from 51 to 193
- Alignment No. 13367
  - gi No. 468605
  - % Identity 74.8
  - Alignment Length 147
  - Location of Alignment in SEQ ID NO 1865: from 48 to 193
- Alignment No. 13368
  - gi No. 4759034
  - % Identity 81.9
  - Alignment Length 149
  - Location of Alignment in SEQ ID NO 1865: from 46 to 193
- Alignment No. 13369
  - gi No. 549010
  - % Identity 91.4
  - Alignment Length 151
  - Location of Alignment in SEQ ID NO 1865: from 44 to 193
- Alignment No. 13370
  - gi No. 549011
  - % Identity 81.9
  - Alignment Length 149
  - Location of Alignment in SEQ ID NO 1865: from 46 to 193
- Alignment No. 13371
  - gi No. 626763
  - % Identity 74.8
  - Alignment Length 147
  - Location of Alignment in SEQ ID NO 1865: from 48 to 193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1866
- Ceres seq\_id 1501545
- Location of start within SEQ ID NO 1864: at 131 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13372
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
- Alignment No. 13373
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150
- Alignment No. 13374
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1866: from 99 to 150
- Alignment No. 13375
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1866: from 8 to 150
- Alignment No. 13376
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
- Alignment No. 13377
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150
- Alignment No. 13378
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1866: from 8 to 150
- Alignment No. 13379
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150
- Alignment No. 13380
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150

- Alignment No. 13381
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1866: from 1 to 150
- Alignment No. 13382
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1866: from 3 to 150
- Alignment No. 13383
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1866: from 5 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1867
- Ceres seq\_id 1501546
- Location of start within SEQ ID NO 1864: at 227 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13384
- gi No. 1155261
- % Identity 90.1
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13385
- gi No. 135054
- % Identity 74.1
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13386
- gi No. 1542845
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 1867: from 67 to 118
- Alignment No. 13387
- gi No. 2315514
- % Identity 79.2
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13388
- gi No. 2996008
- % Identity 80.4
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13389
- gi No. 338687
- % Identity 81.2
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

- Alignment No. 13390
- gi No. 3845214
- % Identity 75.7
- Alignment Length 144
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13391
- gi No. 468605
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13392
- gi No. 4759034
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13393
- gi No. 549010
- % Identity 91.4
- Alignment Length 151
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13394
- gi No. 549011
- % Identity 81.9
- Alignment Length 149
- Location of Alignment in SEQ ID NO 1867: from 1 to 118
- Alignment No. 13395
- gi No. 626763
- % Identity 74.8
- Alignment Length 147
- Location of Alignment in SEQ ID NO 1867: from 1 to 118

Maximum Length Sequence corresponding to clone ID 286066

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1868
- Ceres seq\_id 1501547

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1869
- Ceres seq\_id 1501548
- Location of start within SEQ ID NO 1868: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13396
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1869: from 94 to 241 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13397
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1869: from 91 to 114
- Alignment No. 13398
- gi No. 1304478



- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130
- Alignment No. 13399
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1869: from 91 to 130
- Alignment No. 13400
- gi No. 2129487
- % Identity 81
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1869: from 91 to 243
- Alignment No. 13401
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1869: from 15 to 243
- Alignment No. 13402
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1869: from 15 to 243

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1870
- Ceres seq\_id 1501549
- Location of start within SEQ ID NO 1868: at 17 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13403
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1870: from 89 to 236 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13404
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1870: from 86 to 109
- Alignment No. 13405
- gi No. 1304478
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1870: from 86 to 125
- Alignment No. 13406
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1870: from 86 to 125
- Alignment No. 13407
- gi No. 2129487
- % Identity 81

- Alignment Length 153
- Location of Alignment in SEQ ID NO 1870: from 86 to 238
- Alignment No. 13408
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1870: from 10 to 238
- Alignment No. 13409
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229
- Location of Alignment in SEQ ID NO 1870: from 10 to 238

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1871
- Ceres seq\_id 1501550
- Location of start within SEQ ID NO 1868: at 245 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13410
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 1871: from 13 to 160 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13411
- gi No. 1076713
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1871: from 10 to 33
- Alignment No. 13412
- gi No. 1304478
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1871: from 10 to 49
- Alignment No. 13413
- gi No. 1729427
- % Identity 70
- Alignment Length 40
- Location of Alignment in SEQ ID NO 1871: from 10 to 49
- Alignment No. 13414
- gi No. 2129487
- % Identity 81
- Alignment Length 153
- Location of Alignment in SEQ ID NO 1871: from 10 to 162
- Alignment No. 13415
- gi No. 2829275
- % Identity 71.2
- Alignment Length 230
- Location of Alignment in SEQ ID NO 1871: from 1 to 162
- Alignment No. 13416
- gi No. 4972094
- % Identity 72.5
- Alignment Length 229

- Location of Alignment in SEQ ID NO 1871: from 1 to 162

Maximum Length Sequence corresponding to clone ID 286096

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1872

- Ceres seq\_id 1501565

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1873

- Ceres seq\_id 1501566

- Location of start within SEQ ID NO 1872: at 457 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13417

- gi No. 1002689

- % Identity 72

- Alignment Length 25

- Location of Alignment in SEQ ID NO 1873: from 7 to 31

- Alignment No. 13418

- gi No. 1172600

- % Identity 82.9

- Alignment Length 35

- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13419

- gi No. 130847

- % Identity 78.8

- Alignment Length 33

- Location of Alignment in SEQ ID NO 1873: from 1 to 33

- Alignment No. 13420

- gi No. 130860

- % Identity 88.2

- Alignment Length 34

- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13421

- gi No. 2621771

- % Identity 72

- Alignment Length 25

- Location of Alignment in SEQ ID NO 1873: from 7 to 31

- Alignment No. 13422

- gi No. 2650136

- % Identity 72

- Alignment Length 25

- Location of Alignment in SEQ ID NO 1873: from 7 to 31

- Alignment No. 13423

- gi No. 3080509

- % Identity 73.5

- Alignment Length 34

- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13424

- gi No. 3114275

- % Identity 79.3

- Alignment Length 29

- Location of Alignment in SEQ ID NO 1873: from 5 to 33

- Alignment No. 13425  
- gi No. 3421096  
- % Identity 94.3  
- Alignment Length 35  
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13426  
- gi No. 3914413  
- % Identity 93.9  
- Alignment Length 33  
- Location of Alignment in SEQ ID NO 1873: from 3 to 34

- Alignment No. 13427  
- gi No. 3914424  
- % Identity 91.4  
- Alignment Length 35  
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13428  
- gi No. 3914431  
- % Identity 94.3  
- Alignment Length 35  
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13429  
- gi No. 3914438  
- % Identity 88.2  
- Alignment Length 34  
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13430  
- gi No. 3914440  
- % Identity 71.4  
- Alignment Length 35  
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13431  
- gi No. 4506183  
- % Identity 88.2  
- Alignment Length 34  
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13432  
- gi No. 542655  
- % Identity 88.2  
- Alignment Length 34  
- Location of Alignment in SEQ ID NO 1873: from 1 to 34

- Alignment No. 13433  
- gi No. 585729  
- % Identity 70.8  
- Alignment Length 24  
- Location of Alignment in SEQ ID NO 1873: from 8 to 31

Maximum Length Sequence corresponding to clone ID 286125

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1874
- Ceres seq\_id 1501567

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1875

- Ceres seq\_id 1501568
- Location of start within SEQ ID NO 1874: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1876
- Ceres seq\_id 1501569
- Location of start within SEQ ID NO 1874: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13434
- Ribosomal protein S11
- Location within SEQ ID NO 1876: from 29 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13435
- gi No. 1173200
- % Identity 95.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1876: from 67 to 129

- Alignment No. 13436
- gi No. 1173201
- % Identity 86.5
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1876: from 5 to 129

- Alignment No. 13437
- gi No. 131772
- % Identity 96.9
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13438
- gi No. 131773
- % Identity 94.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1876: from 3 to 129

- Alignment No. 13439
- gi No. 133771
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13440
- gi No. 133777
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13441
- gi No. 133782
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13442  
- gi No. 133785  
- % Identity 84  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13443  
- gi No. 133789  
- % Identity 70.2  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 1876: from 10 to 129

- Alignment No. 13444  
- gi No. 1346941  
- % Identity 76.4  
- Alignment Length 110  
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13445  
- gi No. 1350935  
- % Identity 78.8  
- Alignment Length 132  
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13446  
- gi No. 1350937  
- % Identity 77.9  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13447  
- gi No. 2350992  
- % Identity 76  
- Alignment Length 104  
- Location of Alignment in SEQ ID NO 1876: from 27 to 129

- Alignment No. 13448  
- gi No. 2414647  
- % Identity 80.9  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 1876: from 16 to 129

- Alignment No. 13449  
- gi No. 2500443  
- % Identity 97.8  
- Alignment Length 46  
- Location of Alignment in SEQ ID NO 1876: from 85 to 129

- Alignment No. 13450  
- gi No. 3097244  
- % Identity 85.5  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13451  
- gi No. 3122785  
- % Identity 90  
- Alignment Length 130  
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13452

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- gi No. 4574240
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13453
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13454
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13455
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13456
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13457
- gi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1876: from 72 to 129

- Alignment No. 13458
- gi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13459
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13460
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1876: from 21 to 129

- Alignment No. 13461
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

- Alignment No. 13462
- gi No. 83794

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- % Identity 80
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1876: from 1 to 129

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1877
- Ceres seq\_id 1501570
- Location of start within SEQ ID NO 1874: at 350 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13463
- Ribosomal protein S11
- Location within SEQ ID NO 1877: from 1 to 71 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13464
- gi No. 1173200
- % Identity 95.3
- Alignment Length 64
- Location of Alignment in SEQ ID NO 1877: from 9 to 71

- Alignment No. 13465
- gi No. 1173201
- % Identity 86.5
- Alignment Length 126
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13466
- gi No. 131772
- % Identity 96.9
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13467
- gi No. 131773
- % Identity 94.5
- Alignment Length 128
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13468
- gi No. 133771
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13469
- gi No. 133777
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13470
- gi No. 133782
- % Identity 78.8
- Alignment Length 132
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13471
- gi No. 133785
- % Identity 84

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- Alignment Length 131  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13472  
- gi No. 133789  
- % Identity 70.2  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13473  
- gi No. 1346941  
- % Identity 76.4  
- Alignment Length 110  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13474  
- gi No. 1350935  
- % Identity 78.8  
- Alignment Length 132  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13475  
- gi No. 1350937  
- % Identity 77.9  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13476  
- gi No. 2350992  
- % Identity 76  
- Alignment Length 104  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13477  
- gi No. 2414647  
- % Identity 80.9  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13478  
- gi No. 2500443  
- % Identity 97.8  
- Alignment Length 46  
- Location of Alignment in SEQ ID NO 1877: from 27 to 71

- Alignment No. 13479  
- gi No. 3097244  
- % Identity 85.5  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13480  
- gi No. 3122785  
- % Identity 90  
- Alignment Length 130  
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13481  
- gi No. 4574240  
- % Identity 84.5  
- Alignment Length 110

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- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13482
- gi No. 4588920
- % Identity 81.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13483
- gi No. 4678226
- % Identity 90.8
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13484
- gi No. 4886269
- % Identity 91.5
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13485
- gi No. 5032051
- % Identity 84.7
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13486
- gi No. 5441523
- % Identity 98.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1877: from 14 to 71

- Alignment No. 13487
- gi No. 547604
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13488
- gi No. 70946
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13489
- gi No. 730453
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13490
- gi No. 730633
- % Identity 82.4
- Alignment Length 131
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

- Alignment No. 13491
- gi No. 83794
- % Identity 80
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1877: from 1 to 71

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Maximum Length Sequence corresponding to clone ID 286127

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1878
- Ceres seq\_id 1501571

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1879
- Ceres seq\_id 1501572
- Location of start within SEQ ID NO 1878: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13492
- gi No. 4506093
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1879: from 27 to 37
- Alignment No. 13493
- gi No. 973307
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1879: from 27 to 37

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1880
- Ceres seq\_id 1501573
- Location of start within SEQ ID NO 1878: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13494
- gi No. 2493240
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1880: from 145 to 158
- Alignment No. 13495
- gi No. 4808162
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157
- Alignment No. 13496
- gi No. 4808164
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157
- Alignment No. 13497
- gi No. 4808166
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1880: from 145 to 157
- Alignment No. 13498
- gi No. 4808177
- % Identity 76.9
- Alignment Length 13

- Location of Alignment in SEQ ID NO 1880: from 145 to 157

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 1881
- Ceres seq_id 1501574
- Location of start within SEQ ID NO 1878: at 125 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

- ```

- Alignment No. 13499
- gi No. 2493240
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 1881: from 104 to 117

- Alignment No. 13500
- gi No. 4808162
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116

- Alignment No. 13501
- gi No. 4808164
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116

- Alignment No. 13502
- gi No. 4808166
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116

- Alignment No. 13503
- gi No. 4808177
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 1881: from 104 to 116

```

Maximum Length Sequence corresponding to clone ID 286161

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1882  
- Ceres seq id 1501582

(B) Polypeptide Sequence

- ```
- Pat. Appln. SEQ ID NO 1883
- Ceres seq_id 1501583
- Location of start within SEQ ID NO 1882: at 268 nt.
```

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

#### (D) Related Amino Acid Sequences

- Alignment No. 13504
- gi No. 2655291
- % Identity 84.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1883: from 1 to 76

### (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1884  
- Ceres seq id 1501584

- Location of start within SEQ ID NO 1882: at 352 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13505
- gi No. 2655291
- % Identity 84.4
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1884: from 1 to 48

Maximum Length Sequence corresponding to clone ID 286175

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1885
- Ceres seq\_id 1501589

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1886
- Ceres seq\_id 1501590
- Location of start within SEQ ID NO 1885: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1887
- Ceres seq\_id 1501591
- Location of start within SEQ ID NO 1885: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13506
- Lysyl oxidase
- Location within SEQ ID NO 1887: from 53 to 170 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1888
- Ceres seq\_id 1501592
- Location of start within SEQ ID NO 1885: at 108 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13507
- Lysyl oxidase
- Location within SEQ ID NO 1888: from 18 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286275

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1889
- Ceres seq\_id 1501609

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1890
- Ceres seq\_id 1501610
- Location of start within SEQ ID NO 1889: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1891
- Ceres seq\_id 1501611
- Location of start within SEQ ID NO 1889: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1892
- Ceres seq\_id 1501612
- Location of start within SEQ ID NO 1889: at 324 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13508
- Glycosyl hydrolase family 9
- Location within SEQ ID NO 1892: from 3 to 42 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13509
- gi No. 2765531
- % Identity 76.7
- Alignment Length 30
- Location of Alignment in SEQ ID NO 1892: from 1 to 15

Maximum Length Sequence corresponding to clone ID 286426

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1893
- Ceres seq\_id 1501624

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1894
- Ceres seq\_id 1501625
- Location of start within SEQ ID NO 1893: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13510
- gi No. 2135765
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1894: from 53 to 64

- Alignment No. 13511
- gi No. 4505285
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1894: from 53 to 64

- Alignment No. 13512
- gi No. 542994
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1894: from 21 to 34

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1895

- Ceres seq\_id 1501626
- Location of start within SEQ ID NO 1893: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13513
- gi No. 2224619
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1895: from 58 to 68
- Alignment No. 13514
- gi No. 418612
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1895: from 57 to 68

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1896
- Ceres seq\_id 1501627
- Location of start within SEQ ID NO 1893: at 82 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13515
- gi No. 2135765
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1896: from 26 to 37
- Alignment No. 13516
- gi No. 4505285
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1896: from 26 to 37

Maximum Length Sequence corresponding to clone ID 286438

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1897
- Ceres seq\_id 1501632

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1898
- Ceres seq\_id 1501633
- Location of start within SEQ ID NO 1897: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13517
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1898: from 67 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1899
- Ceres seq\_id 1501634
- Location of start within SEQ ID NO 1897: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13518
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1899: from 28 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1900
- Ceres seq\_id 1501635
- Location of start within SEQ ID NO 1897: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13519
- gi No. 2204081
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 1900: from 19 to 32

Maximum Length Sequence corresponding to clone ID 286538

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1901
- Ceres seq\_id 1501639

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1902
- Ceres seq\_id 1501640
- Location of start within SEQ ID NO 1901: at 165 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1903
- Ceres seq\_id 1501641
- Location of start within SEQ ID NO 1901: at 198 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1904
- Ceres seq\_id 1501642
- Location of start within SEQ ID NO 1901: at 362 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13520
- gi No. 2894559
- % Identity 89.1
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1904: from 1 to 45
- Alignment No. 13521
- gi No. 4115936



- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 1904: from 1 to 45

Maximum Length Sequence corresponding to clone ID 286545

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1905
- Ceres seq\_id 1501643

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1906
- Ceres seq\_id 1501644
- Location of start within SEQ ID NO 1905: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13522
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1906: from 1 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1907
- Ceres seq\_id 1501645
- Location of start within SEQ ID NO 1905: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13523
- Ezrin/radixin/moesin family
- Location within SEQ ID NO 1907: from 1 to 90 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1908
- Ceres seq\_id 1501646
- Location of start within SEQ ID NO 1905: at 399 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286676

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1909
- Ceres seq\_id 1501689

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1910
- Ceres seq\_id 1501690
- Location of start within SEQ ID NO 1909: at 152 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13524
- Ubiquitin family
- Location within SEQ ID NO 1910: from 1 to 74 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1911
- Ceres seq\_id 1501691
- Location of start within SEQ ID NO 1909: at 284 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1912
- Ceres seq\_id 1501692
- Location of start within SEQ ID NO 1909: at 368 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286738

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1913
- Ceres seq\_id 1501701

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1914
- Ceres seq\_id 1501702
- Location of start within SEQ ID NO 1913: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1915
- Ceres seq\_id 1501703
- Location of start within SEQ ID NO 1913: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13525
- gi No. 2244980
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1915: from 31 to 53
- Alignment No. 13526
- gi No. 4587539
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1915: from 31 to 50
- Alignment No. 13527
- gi No. 4914386
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1915: from 31 to 53

Maximum Length Sequence corresponding to clone ID 286767

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1916
- Ceres seq\_id 1501710

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1917
- Ceres seq\_id 1501711
- Location of start within SEQ ID NO 1916: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13528
- Protein phosphatase 2C
- Location within SEQ ID NO 1917: from 32 to 84 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1918
- Ceres seq\_id 1501712
- Location of start within SEQ ID NO 1916: at 295 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13529
- Protein phosphatase 2C
- Location within SEQ ID NO 1918: from 20 to 85 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1919
- Ceres seq\_id 1501713
- Location of start within SEQ ID NO 1916: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13530
- Protein phosphatase 2C
- Location within SEQ ID NO 1919: from 3 to 68 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286773

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1920
- Ceres seq\_id 1501718

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1921
- Ceres seq\_id 1501719
- Location of start within SEQ ID NO 1920: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13531
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13532
- gi No. 1340178
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 1921: from 147 to 168

- Alignment No. 13533
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13534
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13535
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13536
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13537
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1921: from 149 to 168
- Alignment No. 13538
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166
- Alignment No. 13539
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1921: from 149 to 166

(B) Polypeptide Sequence

- Pat. Appl. SEQ ID NO 1922
- Ceres seq\_id 1501720
- Location of start within SEQ ID NO 1920: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13540
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13541
- gi No. 1340178
- % Identity 73.9
- Alignment Length 23

- Location of Alignment in SEQ ID NO 1922: from 131 to 152
- Alignment No. 13542
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13543
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13544
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13545
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13546
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1922: from 133 to 152
- Alignment No. 13547
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150
- Alignment No. 13548
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1922: from 133 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1923
- Ceres seq\_id 1501721
- Location of start within SEQ ID NO 1920: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13549
- gi No. 1093503
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13550
- gi No. 1340178
- % Identity 73.9

- Alignment Length 23
- Location of Alignment in SEQ ID NO 1923: from 73 to 94
- Alignment No. 13551
- gi No. 1498185
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13552
- gi No. 2146900
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13553
- gi No. 416764
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13554
- gi No. 416766
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13555
- gi No. 416767
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 1923: from 75 to 94
- Alignment No. 13556
- gi No. 479893
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92
- Alignment No. 13557
- gi No. 479895
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 1923: from 75 to 92

Maximum Length Sequence corresponding to clone ID 286777

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1924
- Ceres seq\_id 1501722

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1925
- Ceres seq\_id 1501723
- Location of start within SEQ ID NO 1924: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1926
- Ceres seq\_id 1501724

- Location of start within SEQ ID NO 1924: at 41 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1927
- Ceres seq\_id 1501725
- Location of start within SEQ ID NO 1924: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13558
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 1927: from 1 to 55 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 286992

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1928
- Ceres seq\_id 1501730

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1929
- Ceres seq\_id 1501731
- Location of start within SEQ ID NO 1928: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13559
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 33 to 96 aa.
- Alignment No. 13560
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 45 to 102 aa.
- Alignment No. 13561
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 45 to 106 aa.
- Alignment No. 13562
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1929: from 62 to 108 aa.
- Alignment No. 13563
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 100 aa.
- Alignment No. 13564
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 106 aa.
- Alignment No. 13565
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 32 to 108 aa.
- Alignment No. 13566
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 94 aa.

- Alignment No. 13567
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 106 aa.
- Alignment No. 13568
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1929: from 33 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1930
- Ceres seq\_id 1501732
- Location of start within SEQ ID NO 1928: at 347 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1931
- Ceres seq\_id 1501733
- Location of start within SEQ ID NO 1928: at 389 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 287753

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1932
- Ceres seq\_id 1501737

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1933
- Ceres seq\_id 1501738
- Location of start within SEQ ID NO 1932: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1934
- Ceres seq\_id 1501739
- Location of start within SEQ ID NO 1932: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13569
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 1934: from 34 to 83 aa.
- Alignment No. 13570
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1934: from 5 to 83 aa.
- Alignment No. 13571
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 1934: from 21 to 83 aa.



(D) Related Amino Acid Sequences

- Alignment No. 13572
- gi No. 3327046
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1934: from 67 to 83
  
- Alignment No. 13573
- gi No. 3745837
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1934: from 65 to 83
  
- Alignment No. 13574
- gi No. 4028930
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1934: from 67 to 83
  
- Alignment No. 13575
- gi No. 4775349
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13576
- gi No. 4775349
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13577
- gi No. 4996894
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13578
- gi No. 4996894
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1934: from 72 to 82
  
- Alignment No. 13579
- gi No. 688080
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 1934: from 65 to 78

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1935
- Ceres seq\_id 1501740
- Location of start within SEQ ID NO 1932: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 287760

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1936

- Ceres seq\_id 1501741
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1937
  - Ceres seq\_id 1501742
  - Location of start within SEQ ID NO 1936: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13580
- DnaJ domain
- Location within SEQ ID NO 1937: from 36 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13581
- gi No. 1125691
- % Identity 84.5
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13582
- gi No. 1169382
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13583
- gi No. 1169383
- % Identity 76.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13584
- gi No. 1169384
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13585
- gi No. 2129577
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13586
- gi No. 2370312
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13587
- gi No. 2641638
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
  
- Alignment No. 13588
- gi No. 2984709
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

- Alignment No. 13589
- gi No. 39890
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1937: from 37 to 55
- Alignment No. 13590
- gi No. 4008159
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
- Alignment No. 13591
- gi No. 4097575
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
- Alignment No. 13592
- gi No. 4097577
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
- Alignment No. 13593
- gi No. 4210948
- % Identity 91.4
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
- Alignment No. 13594
- gi No. 421809
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
- Alignment No. 13595
- gi No. 4589726
- % Identity 81
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81
- Alignment No. 13596
- gi No. 461942
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 1937: from 45 to 81
- Alignment No. 13597
- gi No. 461944
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1937: from 24 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1938
- Ceres seq\_id 1501743
- Location of start within SEQ ID NO 1936: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

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(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1939
- Ceres seq\_id 1501744
- Location of start within SEQ ID NO 1936: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13598
- DnaJ domain
- Location within SEQ ID NO 1939: from 13 to 58 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13599
- gi No. 1125691
- % Identity 84.5
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13600
- gi No. 1169382
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13601
- gi No. 1169383
- % Identity 76.3
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13602
- gi No. 1169384
- % Identity 86.2
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13603
- gi No. 2129577
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13604
- gi No. 2370312
- % Identity 78
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13605
- gi No. 2641638
- % Identity 79.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1939: from 1 to 58
- Alignment No. 13606
- gi No. 2984709
- % Identity 89.7
- Alignment Length 58
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13607  
- gi No. 39890  
- % Identity 73.7  
- Alignment Length 19  
- Location of Alignment in SEQ ID NO 1939: from 14 to 32

- Alignment No. 13608  
- gi No. 4008159  
- % Identity 89.7  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13609  
- gi No. 4097575  
- % Identity 86.2  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13610  
- gi No. 4097577  
- % Identity 82.8  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13611  
- gi No. 4210948  
- % Identity 91.4  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13612  
- gi No. 421809  
- % Identity 89.7  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13613  
- gi No. 4589726  
- % Identity 81  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

- Alignment No. 13614  
- gi No. 461942  
- % Identity 86.5  
- Alignment Length 37  
- Location of Alignment in SEQ ID NO 1939: from 22 to 58

- Alignment No. 13615  
- gi No. 461944  
- % Identity 89.7  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 1939: from 1 to 58

Maximum Length Sequence corresponding to clone ID 288024

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1940
- Ceres seq\_id 1501755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1941

- Ceres seq\_id 1501756
- Location of start within SEQ ID NO 1940: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1942
- Ceres seq\_id 1501757
- Location of start within SEQ ID NO 1940: at 155 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1943
- Ceres seq\_id 1501758
- Location of start within SEQ ID NO 1940: at 207 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13616
- gi No. 2342735
- % Identity 81.8
- Alignment Length 55
- Location of Alignment in SEQ ID NO 1943: from 37 to 91

Maximum Length Sequence corresponding to clone ID 288145

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1944
- Ceres seq\_id 1501763

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1945
- Ceres seq\_id 1501764
- Location of start within SEQ ID NO 1944: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13617
- Ribosomal protein L14
- Location within SEQ ID NO 1945: from 28 to 149 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13618
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13619
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1945: from 17 to 149
- Alignment No. 13620
- gi No. 1350671
- % Identity 74.8

- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13621  
- gi No. 1350673  
- % Identity 77  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13622  
- gi No. 1710495  
- % Identity 95.4  
- Alignment Length 87  
- Location of Alignment in SEQ ID NO 1945: from 10 to 96

- Alignment No. 13623  
- gi No. 1710496  
- % Identity 75  
- Alignment Length 48  
- Location of Alignment in SEQ ID NO 1945: from 10 to 57

- Alignment No. 13624  
- gi No. 2341028  
- % Identity 96.3  
- Alignment Length 136  
- Location of Alignment in SEQ ID NO 1945: from 14 to 149

- Alignment No. 13625  
- gi No. 2459420  
- % Identity 96.4  
- Alignment Length 140  
- Location of Alignment in SEQ ID NO 1945: from 10 to 149

- Alignment No. 13626  
- gi No. 2500265  
- % Identity 77  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13627  
- gi No. 2706454  
- % Identity 77.4  
- Alignment Length 137  
- Location of Alignment in SEQ ID NO 1945: from 13 to 149

- Alignment No. 13628  
- gi No. 279650  
- % Identity 82.7  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1945: from 10 to 148

- Alignment No. 13629  
- gi No. 2982289  
- % Identity 99.2  
- Alignment Length 133  
- Location of Alignment in SEQ ID NO 1945: from 17 to 149

- Alignment No. 13630  
- gi No. 3851618  
- % Identity 74.6  
- Alignment Length 130

- Location of Alignment in SEQ ID NO 1945: from 20 to 149
- Alignment No. 13631
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1945: from 14 to 138
- Alignment No. 13632
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13633
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149
- Alignment No. 13634
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13635
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1945: from 10 to 148
- Alignment No. 13636
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1945: from 10 to 58
- Alignment No. 13637
- gi No. 730536
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1945: from 10 to 149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1946
- Ceres seq\_id 1501765
- Location of start within SEQ ID NO 1944: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13638
- Ribosomal protein L14
- Location within SEQ ID NO 1946: from 19 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13639
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139



- Alignment No. 13640  
- gi No. 132744  
- % Identity 75.9  
- Alignment Length 133  
- Location of Alignment in SEQ ID NO 1946: from 8 to 140

- Alignment No. 13641  
- gi No. 1350671  
- % Identity 74.8  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13642  
- gi No. 1350673  
- % Identity 77  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13643  
- gi No. 1710495  
- % Identity 95.4  
- Alignment Length 87  
- Location of Alignment in SEQ ID NO 1946: from 1 to 87

- Alignment No. 13644  
- gi No. 1710496  
- % Identity 75  
- Alignment Length 48  
- Location of Alignment in SEQ ID NO 1946: from 1 to 48

- Alignment No. 13645  
- gi No. 2341028  
- % Identity 96.3  
- Alignment Length 136  
- Location of Alignment in SEQ ID NO 1946: from 5 to 140

- Alignment No. 13646  
- gi No. 2459420  
- % Identity 96.4  
- Alignment Length 140  
- Location of Alignment in SEQ ID NO 1946: from 1 to 140

- Alignment No. 13647  
- gi No. 2500265  
- % Identity 77  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13648  
- gi No. 2706454  
- % Identity 77.4  
- Alignment Length 137  
- Location of Alignment in SEQ ID NO 1946: from 4 to 140

- Alignment No. 13649  
- gi No. 279650  
- % Identity 82.7  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1946: from 1 to 139

- Alignment No. 13650
- gi No. 2982289
- % Identity 99.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1946: from 8 to 140
  
- Alignment No. 13651
- gi No. 3851618
- % Identity 74.6
- Alignment Length 130
- Location of Alignment in SEQ ID NO 1946: from 11 to 140
  
- Alignment No. 13652
- gi No. 4028025
- % Identity 83.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 1946: from 5 to 129
  
- Alignment No. 13653
- gi No. 4506605
- % Identity 83.5
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13654
- gi No. 4574244
- % Identity 90
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140
  
- Alignment No. 13655
- gi No. 4583511
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13656
- gi No. 5441537
- % Identity 82.7
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1946: from 1 to 139
  
- Alignment No. 13657
- gi No. 546005
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1946: from 1 to 49
  
- Alignment No. 13658
- gi No. 730536
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1946: from 1 to 140

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1947
- Ceres seq\_id 1501766
- Location of start within SEQ ID NO 1944: at 74 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13659
- Ribosomal protein L14
- Location within SEQ ID NO 1947: from 4 to 125 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13660
- gi No. 103355
- % Identity 79.9
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13661
- gi No. 132744
- % Identity 75.9
- Alignment Length 133
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13662
- gi No. 1350671
- % Identity 74.8
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13663
- gi No. 1350673
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13664
- gi No. 1710495
- % Identity 95.4
- Alignment Length 87
- Location of Alignment in SEQ ID NO 1947: from 1 to 72
- Alignment No. 13665
- gi No. 1710496
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 1947: from 1 to 33
- Alignment No. 13666
- gi No. 2341028
- % Identity 96.3
- Alignment Length 136
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13667
- gi No. 2459420
- % Identity 96.4
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125
- Alignment No. 13668
- gi No. 2500265
- % Identity 77
- Alignment Length 139
- Location of Alignment in SEQ ID NO 1947: from 1 to 124
- Alignment No. 13669
- gi No. 2706454

- % Identity 77.4  
- Alignment Length 137  
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13670  
- gi No. 279650  
- % Identity 82.7  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13671  
- gi No. 2982289  
- % Identity 99.2  
- Alignment Length 133  
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13672  
- gi No. 3851618  
- % Identity 74.6  
- Alignment Length 130  
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13673  
- gi No. 4028025  
- % Identity 83.2  
- Alignment Length 125  
- Location of Alignment in SEQ ID NO 1947: from 1 to 114

- Alignment No. 13674  
- gi No. 4506605  
- % Identity 83.5  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13675  
- gi No. 4574244  
- % Identity 90  
- Alignment Length 140  
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

- Alignment No. 13676  
- gi No. 4583511  
- % Identity 82.7  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13677  
- gi No. 5441537  
- % Identity 82.7  
- Alignment Length 139  
- Location of Alignment in SEQ ID NO 1947: from 1 to 124

- Alignment No. 13678  
- gi No. 546005  
- % Identity 75.5  
- Alignment Length 49  
- Location of Alignment in SEQ ID NO 1947: from 1 to 34

- Alignment No. 13679  
- gi No. 730536  
- % Identity 96.4

- Alignment Length 140
- Location of Alignment in SEQ ID NO 1947: from 1 to 125

Maximum Length Sequence corresponding to clone ID 288149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1948
- Ceres seq\_id 1501771

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1949
- Ceres seq\_id 1501772
- Location of start within SEQ ID NO 1948: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1949: from 88 to 176 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1950
- Ceres seq\_id 1501773
- Location of start within SEQ ID NO 1948: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13681
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1950: from 43 to 131 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1951
- Ceres seq\_id 1501774
- Location of start within SEQ ID NO 1948: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13682
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 1951: from 8 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 288431

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1952
- Ceres seq\_id 1501786

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1953
- Ceres seq\_id 1501787
- Location of start within SEQ ID NO 1952: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13683
- gi No. 1184100
- % Identity 90.9

- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50
- Alignment No. 13684
- gi No. 1914851
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 41 to 51
- Alignment No. 13685
- gi No. 688080
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1953: from 40 to 50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1954
- Ceres seq\_id 1501788
- Location of start within SEQ ID NO 1952: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13686
- gi No. 19917
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1954: from 30 to 40
- Alignment No. 13687
- gi No. 322760
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1954: from 30 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1955
- Ceres seq\_id 1501789
- Location of start within SEQ ID NO 1952: at 26 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13688
- gi No. 19917
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 1955: from 22 to 32
- Alignment No. 13689
- gi No. 322760
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 1955: from 22 to 32

Maximum Length Sequence corresponding to clone ID 288440

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1956
- Ceres seq\_id 1501794

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1957

- Ceres seq\_id 1501795
- Location of start within SEQ ID NO 1956: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1958
- Ceres seq\_id 1501796
- Location of start within SEQ ID NO 1956: at 182 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13690
- gi No. 4521249
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

- Alignment No. 13691
- gi No. 4587311
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

- Alignment No. 13692
- gi No. 4929561
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1958: from 1 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1959
- Ceres seq\_id 1501797
- Location of start within SEQ ID NO 1956: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13693
- gi No. 4521249
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

- Alignment No. 13694
- gi No. 4587311
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

- Alignment No. 13695
- gi No. 4929561
- % Identity 71
- Alignment Length 107
- Location of Alignment in SEQ ID NO 1959: from 1 to 83

Maximum Length Sequence corresponding to clone ID 288752

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1960
- Ceres seq\_id 1501804
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1961
  - Ceres seq\_id 1501805
  - Location of start within SEQ ID NO 1960: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13696
  - gi No. 1076501
  - % Identity 75
  - Alignment Length 12
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13697
  - gi No. 1076501
  - % Identity 76.9
  - Alignment Length 13
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13698
  - gi No. 1155068
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13699
  - gi No. 1155068
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 1961: from 62 to 73
- Alignment No. 13700
  - gi No. 1155068
  - % Identity 70.6
  - Alignment Length 17
  - Location of Alignment in SEQ ID NO 1961: from 62 to 74
- Alignment No. 13701
  - gi No. 1155068
  - % Identity 70.6
  - Alignment Length 17
  - Location of Alignment in SEQ ID NO 1961: from 62 to 74
- Alignment No. 13702
  - gi No. 2226329
  - % Identity 84.7
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 1961: from 34 to 91
- Alignment No. 13703
  - gi No. 399204
  - % Identity 86.4
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 1961: from 34 to 91
- Alignment No. 13704
  - gi No. 688422
  - % Identity 71.4



- Alignment Length 14
- Location of Alignment in SEQ ID NO 1961: from 79 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1962
- Ceres seq\_id 1501806
- Location of start within SEQ ID NO 1960: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13705
- Plant lipid transfer protein family
- Location within SEQ ID NO 1962: from 81 to 137 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13706
- gi No. 1092083
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 1962: from 112 to 128

- Alignment No. 13707
- gi No. 2226329
- % Identity 82
- Alignment Length 50
- Location of Alignment in SEQ ID NO 1962: from 89 to 136

- Alignment No. 13708
- gi No. 399204
- % Identity 81.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 1962: from 89 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1963
- Ceres seq\_id 1501807
- Location of start within SEQ ID NO 1960: at 158 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 288760

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1964
- Ceres seq\_id 1501810

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1965
- Ceres seq\_id 1501811
- Location of start within SEQ ID NO 1964: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13709
- gi No. 1076418
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13710

- gi No. 1717779
- % Identity 70.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 9 to 109
- Alignment No. 13711
- gi No. 1942055
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13712
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1965: from 10 to 109
- Alignment No. 13713
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1965: from 12 to 105
- Alignment No. 13714
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1965: from 11 to 109
- Alignment No. 13715
- gi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1965: from 34 to 109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1966
- Ceres seq\_id 1501812
- Location of start within SEQ ID NO 1964: at 241 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13716
- gi No. 1076418
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13717
- gi No. 1717779
- % Identity 70.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13718
- gi No. 1942055
- % Identity 77
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67

- Alignment No. 13719
- gi No. 2262173
- % Identity 72.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13720
- gi No. 2500128
- % Identity 70.2
- Alignment Length 94
- Location of Alignment in SEQ ID NO 1966: from 1 to 63
- Alignment No. 13721
- gi No. 2500129
- % Identity 71
- Alignment Length 100
- Location of Alignment in SEQ ID NO 1966: from 1 to 67
- Alignment No. 13722
- gi No. 2500130
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 1966: from 1 to 67

Maximum Length Sequence corresponding to clone ID 288771

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1967
- Ceres seq\_id 1501813

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1968
- Ceres seq\_id 1501814
- Location of start within SEQ ID NO 1967: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13723
- gi No. 3128181
- % Identity 74.6
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1968: from 42 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1969
- Ceres seq\_id 1501815
- Location of start within SEQ ID NO 1967: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1970
- Ceres seq\_id 1501816
- Location of start within SEQ ID NO 1967: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13724
- gi No. 3128181

- % Identity 74.6
- Alignment Length 59
- Location of Alignment in SEQ ID NO 1970: from 1 to 59

Maximum Length Sequence corresponding to clone ID 289873

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1971
- Ceres seq\_id 1501824

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1972
- Ceres seq\_id 1501825
- Location of start within SEQ ID NO 1971: at 304 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13725
- GDP dissociation inhibitor
- Location within SEQ ID NO 1972: from 1 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13726
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1972: from 1 to 100
- Alignment No. 13727
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1972: from 1 to 100
- Alignment No. 13728
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1972: from 1 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1973
- Ceres seq\_id 1501826
- Location of start within SEQ ID NO 1971: at 319 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13729
- GDP dissociation inhibitor
- Location within SEQ ID NO 1973: from 1 to 95 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13730
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1973: from 1 to 95
- Alignment No. 13731
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1973: from 1 to 95

- Alignment No. 13732
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1973: from 1 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1974
- Ceres seq\_id 1501827
- Location of start within SEQ ID NO 1971: at 322 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13733
- GDP dissociation inhibitor
- Location within SEQ ID NO 1974: from 1 to 94 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13734
- gi No. 2384758
- % Identity 70.1
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1974: from 1 to 94

- Alignment No. 13735
- gi No. 2384760
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 1974: from 1 to 94

- Alignment No. 13736
- gi No. 2501850
- % Identity 74.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 1974: from 1 to 94

Maximum Length Sequence corresponding to clone ID 289892

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1975
- Ceres seq\_id 1501828

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1976
- Ceres seq\_id 1501829
- Location of start within SEQ ID NO 1975: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13737
- gi No. 3860272
- % Identity 85.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1976: from 62 to 163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1977
- Ceres seq\_id 1501830
- Location of start within SEQ ID NO 1975: at 186 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13738
- gi No. 3860272
- % Identity 85.6
- Alignment Length 105
- Location of Alignment in SEQ ID NO 1977: from 1 to 102

Maximum Length Sequence corresponding to clone ID 291908

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1978
- Ceres seq\_id 1501850

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1979
- Ceres seq\_id 1501851
- Location of start within SEQ ID NO 1978: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1980
- Ceres seq\_id 1501852
- Location of start within SEQ ID NO 1978: at 12 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1981
- Ceres seq\_id 1501853
- Location of start within SEQ ID NO 1978: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13739
- Thioredoxin
- Location within SEQ ID NO 1981: from 31 to 139 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13740
- gi No. 1848212
- % Identity 75.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1981: from 7 to 143
- Alignment No. 13741
- gi No. 2529680
- % Identity 74.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 1981: from 7 to 143
- Alignment No. 13742
- gi No. 729442
- % Identity 74.3
- Alignment Length 140
- Location of Alignment in SEQ ID NO 1981: from 5 to 143

- Alignment No. 13743
- gi No. 99991
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 1981: from 52 to 70
- Alignment No. 13744
- gi No. 99991
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 1981: from 51 to 70

Maximum Length Sequence corresponding to clone ID 292482

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1982
- Ceres seq\_id 1501862

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1983
- Ceres seq\_id 1501863
- Location of start within SEQ ID NO 1982: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1984
- Ceres seq\_id 1501864
- Location of start within SEQ ID NO 1982: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13745
- Ribosomal protein L13e
- Location within SEQ ID NO 1984: from 6 to 82 aa.
- Alignment No. 13746
- Fatty acid desaturase
- Location within SEQ ID NO 1984: from 77 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13747
- gi No. 1350664
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1984: from 10 to 82
- Alignment No. 13748
- gi No. 2662188
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1984: from 1 to 84
- Alignment No. 13749
- gi No. 730449
- % Identity 86.9
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1984: from 2 to 84
- Alignment No. 13750
- gi No. 730450

- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 62
- Alignment No. 13751
- gi No. 730526
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1984: from 2 to 82

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1985
- Ceres seq\_id 1501865
- Location of start within SEQ ID NO 1982: at 274 nt.

(C) Nominatation and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13752
- Fatty acid desaturase
- Location within SEQ ID NO 1985: from 11 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13753
- gi No. 1350664
- % Identity 89
- Alignment Length 73
- Location of Alignment in SEQ ID NO 1985: from 1 to 16
- Alignment No. 13754
- gi No. 2662188
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 1985: from 1 to 18
- Alignment No. 13755
- gi No. 730449
- % Identity 86.9
- Alignment Length 84
- Location of Alignment in SEQ ID NO 1985: from 1 to 18
- Alignment No. 13756
- gi No. 730450
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1985: from 1 to 16
- Alignment No. 13757
- gi No. 730526
- % Identity 88.9
- Alignment Length 81
- Location of Alignment in SEQ ID NO 1985: from 1 to 16

Maximum Length Sequence corresponding to clone ID 293228

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1986
- Ceres seq\_id 1501872

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1987
- Ceres seq\_id 1501873
- Location of start within SEQ ID NO 1986: at 3 nt.



(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1988
- Ceres seq\_id 1501874
- Location of start within SEQ ID NO 1986: at 92 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13758
- Oleosin
- Location within SEQ ID NO 1988: from 1 to 78 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1989
- Ceres seq\_id 1501875
- Location of start within SEQ ID NO 1986: at 161 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13759
- Oleosin
- Location within SEQ ID NO 1989: from 1 to 55 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293659

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1990
- Ceres seq\_id 1501884

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1991
- Ceres seq\_id 1501885
- Location of start within SEQ ID NO 1990: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1992
- Ceres seq\_id 1501886
- Location of start within SEQ ID NO 1990: at 217 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13760
- gi No. 166410
- % Identity 78.8
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1992: from 1 to 112
- Alignment No. 13761
- gi No. 3894178
- % Identity 81.4
- Alignment Length 102

- Location of Alignment in SEQ ID NO 1992: from 12 to 112
- Alignment No. 13762
- gi No. 4091080
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13763
- gi No. 4091117
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1992: from 3 to 112
- Alignment No. 13764
- gi No. 4884860
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1992: from 3 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 1993
- Ceres seq id 1501887
- Location of start within SEQ ID NO 1990: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13765
- gi No. 166410
- % Identity 78.8
- Alignment Length 113
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13766
- gi No. 3894178
- % Identity 81.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13767
- gi No. 4091080
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13768
- gi No. 4091117
- % Identity 79.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 1993: from 1 to 69
- Alignment No. 13769
- gi No. 4884860
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 1993: from 1 to 69

Maximum Length Sequence corresponding to clone ID 293683

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1994

- Ceres seq\_id 1501888
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1995
  - Ceres seq\_id 1501889
  - Location of start within SEQ ID NO 1994: at 203 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13770
- Aminotransferases class-I
- Location within SEQ ID NO 1995: from 16 to 109 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1996
  - Ceres seq\_id 1501890
  - Location of start within SEQ ID NO 1994: at 257 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13771
- Aminotransferases class-I
- Location within SEQ ID NO 1996: from 1 to 91 aa.

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1997
  - Ceres seq\_id 1501891
  - Location of start within SEQ ID NO 1994: at 299 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13772
- Aminotransferases class-I
- Location within SEQ ID NO 1997: from 1 to 77 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293689

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 1998
  - Ceres seq\_id 1501895
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 1999
  - Ceres seq\_id 1501896
  - Location of start within SEQ ID NO 1998: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13773
- DnaJ domain
- Location within SEQ ID NO 1999: from 5 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13774
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 1999: from 13 to 47

- Alignment No. 13775
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 1999: from 24 to 47

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2000
- Ceres seq\_id 1501897
- Location of start within SEQ ID NO 1998: at 29 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13776
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2000: from 4 to 38
- Alignment No. 13777
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2000: from 15 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2001
- Ceres seq\_id 1501898
- Location of start within SEQ ID NO 1998: at 86 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13778
- gi No. 126757
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2001: from 1 to 19
- Alignment No. 13779
- gi No. 30851
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2001: from 1 to 19

Maximum Length Sequence corresponding to clone ID 293692

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2002
- Ceres seq\_id 1501899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2003
- Ceres seq\_id 1501900
- Location of start within SEQ ID NO 2002: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13780
- Pyruvate kinase
- Location within SEQ ID NO 2003: from 110 to 143 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13781
- gi No. 125606
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143
  
- Alignment No. 13782
- gi No. 2497538
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143
  
- Alignment No. 13783
- gi No. 2497543
- % Identity 91.7
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2003: from 109 to 143
  
- Alignment No. 13784
- gi No. 322787
- % Identity 90
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2003: from 105 to 143
  
- Alignment No. 13785
- gi No. 4033431
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2003: from 109 to 143

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2004
- Ceres seq\_id 1501901
- Location of start within SEQ ID NO 2002: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13786
- gi No. 2134206
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2004: from 53 to 63

Maximum Length Sequence corresponding to clone ID 293697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2005
- Ceres seq\_id 1501902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2006
- Ceres seq\_id 1501903
- Location of start within SEQ ID NO 2005: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13787
- gi No. 1947160
- % Identity 72.7

- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34
- Alignment No. 13788
- gi No. 3858883
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 18 to 28
- Alignment No. 13789
- gi No. 4996894
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2006: from 24 to 34

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2007
- Ceres seq\_id 1501904
- Location of start within SEQ ID NO 2005: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13790
- Syndecan domain
- Location within SEQ ID NO 2007: from 39 to 141 aa.
- Alignment No. 13791
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2007: from 24 to 139 aa.
- Alignment No. 13792
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 35 to 140 aa.
- Alignment No. 13793
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 35 to 141 aa.
- Alignment No. 13794
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 41 to 139 aa.
- Alignment No. 13795
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 59 to 139 aa.
- Alignment No. 13796
- Mucin-like glycoprotein
- Location within SEQ ID NO 2007: from 76 to 139 aa.
- Alignment No. 13797
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2007: from 21 to 137 aa.
- Alignment No. 13798
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2007: from 21 to 141 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13799
- gi No. 585527

- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2007: from 128 to 141

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2008
- Ceres seq\_id 1501905
- Location of start within SEQ ID NO 2005: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13800
- gi No. 113928
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2008: from 7 to 18
  
- Alignment No. 13801
- gi No. 1914853
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2008: from 18 to 28
  
- Alignment No. 13802
- gi No. 2077900
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2008: from 17 to 27
  
- Alignment No. 13803
- gi No. 280655
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2008: from 7 to 18

Maximum Length Sequence corresponding to clone ID 293718

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2009
- Ceres seq\_id 1501906

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2010
- Ceres seq\_id 1501907
- Location of start within SEQ ID NO 2009: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13804
- gi No. 2909522
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2010: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2011
- Ceres seq\_id 1501908
- Location of start within SEQ ID NO 2009: at 388 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2012
- Ceres seq\_id 1501909
- Location of start within SEQ ID NO 2009: at 407 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2013
- Ceres seq\_id 1501922

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2014
- Ceres seq\_id 1501923
- Location of start within SEQ ID NO 2013: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13805
- Peroxidase
- Location within SEQ ID NO 2014: from 48 to 113 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2015
- Ceres seq\_id 1501924
- Location of start within SEQ ID NO 2013: at 223 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13806
- Peroxidase
- Location within SEQ ID NO 2015: from 43 to 108 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2016
- Ceres seq\_id 1501925
- Location of start within SEQ ID NO 2013: at 226 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13807
- Peroxidase
- Location within SEQ ID NO 2016: from 42 to 107 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293858

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2017
- Ceres seq\_id 1501926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2018
- Ceres seq\_id 1501927



- Location of start within SEQ ID NO 2017: at 190 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13808
- Synaptobrevin
- Location within SEQ ID NO 2018: from 62 to 121 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13809
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2018: from 62 to 121

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2019
- Ceres seq\_id 1501928
- Location of start within SEQ ID NO 2017: at 205 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13810
- Synaptobrevin
- Location within SEQ ID NO 2019: from 57 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13811
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2019: from 57 to 116

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2020
- Ceres seq\_id 1501929
- Location of start within SEQ ID NO 2017: at 346 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13812
- Synaptobrevin
- Location within SEQ ID NO 2020: from 10 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13813
- gi No. 3157951
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2020: from 10 to 69

Maximum Length Sequence corresponding to clone ID 293863

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2021
- Ceres seq\_id 1501930

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2022
- Ceres seq\_id 1501931
- Location of start within SEQ ID NO 2021: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2023
- Ceres seq\_id 1501932
- Location of start within SEQ ID NO 2021: at 97 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13814
- gi No. 2213626
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2023: from 9 to 27
- Alignment No. 13815
- gi No. 4850408
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2023: from 13 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2024
- Ceres seq\_id 1501933
- Location of start within SEQ ID NO 2021: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 293882

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2025
- Ceres seq\_id 1501949

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2026
- Ceres seq\_id 1501950
- Location of start within SEQ ID NO 2025: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2027
- Ceres seq\_id 1501951
- Location of start within SEQ ID NO 2025: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2028
- Ceres seq\_id 1501952
- Location of start within SEQ ID NO 2025: at 96 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13816
- ABC transporter
- Location within SEQ ID NO 2028: from 83 to 147 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297023

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2029
- Ceres seq\_id 1501976

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2030
- Ceres seq\_id 1501977
- Location of start within SEQ ID NO 2029: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2031
- Ceres seq\_id 1501978
- Location of start within SEQ ID NO 2029: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13817
- gi No. 4678325
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2031: from 41 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2032
- Ceres seq\_id 1501979
- Location of start within SEQ ID NO 2029: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13818
- gi No. 4678325
- % Identity 78.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2032: from 17 to 86

Maximum Length Sequence corresponding to clone ID 297685

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2033
- Ceres seq\_id 1502003

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2034
- Ceres seq\_id 1502004
- Location of start within SEQ ID NO 2033: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2035
- Ceres seq\_id 1502005
- Location of start within SEQ ID NO 2033: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13819
- Gag polyprotein, inner coat protein p12
- Location within SEQ ID NO 2035: from 35 to 89 aa.
- Alignment No. 13820
- Mucin-like glycoprotein
- Location within SEQ ID NO 2035: from 12 to 130 aa.
- Alignment No. 13821
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 27 to 85 aa.
- Alignment No. 13822
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 27 to 93 aa.
- Alignment No. 13823
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 33 to 116 aa.
- Alignment No. 13824
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2035: from 34 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13825
- gi No. 2134206
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13826
- gi No. 2134208
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13827
- gi No. 2134209
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 136 to 146
- Alignment No. 13828
- gi No. 2507155
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13829
- gi No. 439289
- % Identity 72.7
- Alignment Length 11

- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13830
- gi No. 871535
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2035: from 45 to 55
- Alignment No. 13831
- gi No. 93144
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2035: from 32 to 52
- Alignment No. 13832
- gi No. 93144
- % Identity 73.9
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2035: from 32 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2036
- Ceres seq\_id 1502006
- Location of start within SEQ ID NO 2033: at 116 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297707

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2037
- Ceres seq\_id 1502011

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2038
- Ceres seq\_id 1502012
- Location of start within SEQ ID NO 2037: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13833
- gi No. 3915131
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2038: from 24 to 61

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2039
- Ceres seq\_id 1502013
- Location of start within SEQ ID NO 2037: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13834
- GMC oxidoreductases
- Location within SEQ ID NO 2039: from 1 to 55 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13835
- gi No. 4903006

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- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63
- Alignment No. 13836
- gi No. 4903018
- % Identity 71.4
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2039: from 1 to 63

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2040
- Ceres seq\_id 1502014
- Location of start within SEQ ID NO 2037: at 575 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297709

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2041
- Ceres seq\_id 1502015

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2042
- Ceres seq\_id 1502016
- Location of start within SEQ ID NO 2041: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2043
- Ceres seq\_id 1502017
- Location of start within SEQ ID NO 2041: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13837
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2043: from 41 to 54
- Alignment No. 13838
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2043: from 41 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2044
- Ceres seq\_id 1502018
- Location of start within SEQ ID NO 2041: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13839

- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29
- Alignment No. 13840
- gi No. 82087
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2044: from 16 to 29

Maximum Length Sequence corresponding to clone ID 297786

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2045
- Ceres seq\_id 1502023

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2046
- Ceres seq\_id 1502024
- Location of start within SEQ ID NO 2045: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13841
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2046: from 78 to 129 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2047
- Ceres seq\_id 1502025
- Location of start within SEQ ID NO 2045: at 289 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2048
- Ceres seq\_id 1502026
- Location of start within SEQ ID NO 2045: at 298 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 297797

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2049
- Ceres seq\_id 1502027

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2050
- Ceres seq\_id 1502028
- Location of start within SEQ ID NO 2049: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2051

- Ceres seq\_id 1502029
- Location of start within SEQ ID NO 2049: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2052
- Ceres seq\_id 1502030
- Location of start within SEQ ID NO 2049: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13842
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2052: from 1 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13843
- gi No. 1174852
- % Identity 78.9
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2052: from 7 to 81
- Alignment No. 13844
- gi No. 136647
- % Identity 86.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2052: from 23 to 81
- Alignment No. 13845
- gi No. 2129758
- % Identity 83.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2052: from 6 to 81
- Alignment No. 13846
- gi No. 2624417
- % Identity 98.8
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2052: from 1 to 81
- Alignment No. 13847
- gi No. 2641619
- % Identity 89
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2052: from 1 to 81
- Alignment No. 13848
- gi No. 992706
- % Identity 80.5
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2052: from 6 to 81

Maximum Length Sequence corresponding to clone ID 297802

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2053
- Ceres seq\_id 1502031

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2054



- Ceres seq\_id 1502032
- Location of start within SEQ ID NO 2053: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13849
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2054: from 110 to 174 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13850
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2054: from 35 to 174
- Alignment No. 13851
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2054: from 22 to 174
- Alignment No. 13852
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2054: from 29 to 174
- Alignment No. 13853
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174
- Alignment No. 13854
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2054: from 84 to 174
- Alignment No. 13855
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2054: from 53 to 174
- Alignment No. 13856
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174
- Alignment No. 13857
- gi No. 399785
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2054: from 53 to 174
- Alignment No. 13858
- gi No. 97570
- % Identity 75

- Alignment Length 104
- Location of Alignment in SEQ ID NO 2054: from 72 to 174

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2055
- Ceres seq\_id 1502033
- Location of start within SEQ ID NO 2053: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13859
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2055: from 89 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13860
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2055: from 14 to 153
- Alignment No. 13861
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2055: from 1 to 153
- Alignment No. 13862
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2055: from 8 to 153
- Alignment No. 13863
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153
- Alignment No. 13864
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2055: from 63 to 153
- Alignment No. 13865
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2055: from 32 to 153
- Alignment No. 13866
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153
- Alignment No. 13867
- gi No. 399785
- % Identity 78
- Alignment Length 123

- Location of Alignment in SEQ ID NO 2055: from 32 to 153
- Alignment No. 13868
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2055: from 51 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2056
- Ceres seq\_id 1502034
- Location of start within SEQ ID NO 2053: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13869
- Aminotransferases class-III pyridoxal-phosphate
- Location within SEQ ID NO 2056: from 69 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13870
- gi No. 100332
- % Identity 70.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13871
- gi No. 1170029
- % Identity 85.7
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13872
- gi No. 1170031
- % Identity 71.4
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2056: from 1 to 133
- Alignment No. 13873
- gi No. 1170032
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133
- Alignment No. 13874
- gi No. 2492858
- % Identity 76.1
- Alignment Length 92
- Location of Alignment in SEQ ID NO 2056: from 43 to 133
- Alignment No. 13875
- gi No. 2492862
- % Identity 77.2
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2056: from 12 to 133
- Alignment No. 13876
- gi No. 2982001
- % Identity 74
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133

- Alignment No. 13877
- gi No. 399785
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2056: from 12 to 133
- Alignment No. 13878
- gi No. 97570
- % Identity 75
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2056: from 31 to 133

Maximum Length Sequence corresponding to clone ID 297826

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2057
- Ceres seq\_id 1502035

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2058
- Ceres seq\_id 1502036
- Location of start within SEQ ID NO 2057: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13879
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2058: from 67 to 119 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2059
- Ceres seq\_id 1502037
- Location of start within SEQ ID NO 2057: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13880
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2059: from 65 to 117 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2060
- Ceres seq\_id 1502038
- Location of start within SEQ ID NO 2057: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13881
- Bowman-Birk serine protease inhibitor family
- Location within SEQ ID NO 2060: from 57 to 109 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298533

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2061
- Ceres seq\_id 1502048

(B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 2062
- Ceres seq\_id 1502049
- Location of start within SEQ ID NO 2061: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2063
- Ceres seq\_id 1502050
- Location of start within SEQ ID NO 2061: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13882
- Sugar (and other) transporter
- Location within SEQ ID NO 2063: from 26 to 175 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2064
- Ceres seq\_id 1502056

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2065
- Ceres seq\_id 1502057
- Location of start within SEQ ID NO 2064: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2066
- Ceres seq\_id 1502058
- Location of start within SEQ ID NO 2064: at 330 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13883
- gi No. 3402683
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2066: from 22 to 48
- Alignment No. 13884
- gi No. 4678298
- % Identity 95.7
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2066: from 22 to 44
- Alignment No. 13885
- gi No. 4914404
- % Identity 79.3
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2066: from 24 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2067
- Ceres seq\_id 1502059
- Location of start within SEQ ID NO 2064: at 348 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13886
- gi No. 3402683
- % Identity 81.5
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2067: from 16 to 42
- Alignment No. 13887
- gi No. 4678298
- % Identity 95.7
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2067: from 16 to 38
- Alignment No. 13888
- gi No. 4914404
- % Identity 79.3
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2067: from 18 to 46

Maximum Length Sequence corresponding to clone ID 298567

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2068
- Ceres seq\_id 1502066

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2069
- Ceres seq\_id 1502067
- Location of start within SEQ ID NO 2068: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13889
- DnaJ domain
- Location within SEQ ID NO 2069: from 12 to 79 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 298580

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2070
- Ceres seq\_id 1502074

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2071
- Ceres seq\_id 1502075
- Location of start within SEQ ID NO 2070: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13890
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2071: from 70 to 120 aa.
- Alignment No. 13891
- Mucin-like glycoprotein
- Location within SEQ ID NO 2071: from 34 to 153 aa.

- Alignment No. 13892
  - Mucin-like glycoprotein
  - Location within SEQ ID NO 2071: from 58 to 148 aa.
  - Alignment No. 13893
  - Mucin-like glycoprotein
  - Location within SEQ ID NO 2071: from 58 to 151 aa.
  - Alignment No. 13894
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 41 to 153 aa.
  - Alignment No. 13895
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 48 to 153 aa.
  - Alignment No. 13896
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 59 to 134 aa.
  - Alignment No. 13897
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 61 to 116 aa.
  - Alignment No. 13898
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 61 to 140 aa.
  - Alignment No. 13899
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 61 to 147 aa.
  - Alignment No. 13900
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 61 to 150 aa.
  - Alignment No. 13901
  - 7 transmembrane receptor (rhodopsin family)
  - Location within SEQ ID NO 2071: from 61 to 153 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 13902
  - gi No. 100687
  - % Identity 70.6
  - Alignment Length 138
  - Location of Alignment in SEQ ID NO 2071: from 32 to 153
  - Alignment No. 13903
  - gi No. 228937
  - % Identity 91.5
  - Alignment Length 136
  - Location of Alignment in SEQ ID NO 2071: from 28 to 153
  - Alignment No. 13904
  - gi No. 228938
  - % Identity 93.3
  - Alignment Length 134
  - Location of Alignment in SEQ ID NO 2071: from 28 to 153
  - Alignment No. 13905
  - gi No. 283032

- % Identity 96.2
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
  
- Alignment No. 13906
- gi No. 283045
- % Identity 91.9
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2071: from 28 to 153
  
- Alignment No. 13907
- gi No. 458468
- % Identity 71.8
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 107 to 141
  
- Alignment No. 13908
- gi No. 458468
- % Identity 75.7
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2071: from 118 to 153
  
- Alignment No. 13909
- gi No. 458468
- % Identity 76.3
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2071: from 112 to 149
  
- Alignment No. 13910
- gi No. 458468
- % Identity 75
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
  
- Alignment No. 13911
- gi No. 458468
- % Identity 72.5
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2071: from 112 to 151
  
- Alignment No. 13912
- gi No. 458468
- % Identity 71.4
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2071: from 107 to 148
  
- Alignment No. 13913
- gi No. 82698
- % Identity 91.6
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2071: from 28 to 153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2072
- Ceres seq\_id 1502076
- Location of start within SEQ ID NO 2070: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13914
- Collagen triple helix repeat (20 copies)



- Location within SEQ ID NO 2072: from 44 to 94 aa.
- Alignment No. 13915
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 8 to 127 aa.
- Alignment No. 13916
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 122 aa.
- Alignment No. 13917
- Mucin-like glycoprotein
- Location within SEQ ID NO 2072: from 32 to 125 aa.
- Alignment No. 13918
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 15 to 127 aa.
- Alignment No. 13919
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 22 to 127 aa.
- Alignment No. 13920
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 33 to 108 aa.
- Alignment No. 13921
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 90 aa.
- Alignment No. 13922
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 114 aa.
- Alignment No. 13923
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 121 aa.
- Alignment No. 13924
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 124 aa.
- Alignment No. 13925
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2072: from 35 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13926
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2072: from 6 to 127
- Alignment No. 13927
- gi No. 228937
- % Identity 91.5
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2072: from 2 to 127
- Alignment No. 13928
- gi No. 228938

- % Identity 93.3  
- Alignment Length 134  
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

- Alignment No. 13929  
- gi No. 283032  
- % Identity 96.2  
- Alignment Length 130  
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

- Alignment No. 13930  
- gi No. 283045  
- % Identity 91.9  
- Alignment Length 136  
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

- Alignment No. 13931  
- gi No. 458468  
- % Identity 71.8  
- Alignment Length 39  
- Location of Alignment in SEQ ID NO 2072: from 81 to 115

- Alignment No. 13932  
- gi No. 458468  
- % Identity 75.7  
- Alignment Length 39  
- Location of Alignment in SEQ ID NO 2072: from 92 to 127

- Alignment No. 13933  
- gi No. 458468  
- % Identity 76.3  
- Alignment Length 40  
- Location of Alignment in SEQ ID NO 2072: from 86 to 123

- Alignment No. 13934  
- gi No. 458468  
- % Identity 75  
- Alignment Length 43  
- Location of Alignment in SEQ ID NO 2072: from 86 to 125

- Alignment No. 13935  
- gi No. 458468  
- % Identity 72.5  
- Alignment Length 43  
- Location of Alignment in SEQ ID NO 2072: from 86 to 125

- Alignment No. 13936  
- gi No. 458468  
- % Identity 71.4  
- Alignment Length 44  
- Location of Alignment in SEQ ID NO 2072: from 81 to 122

- Alignment No. 13937  
- gi No. 82698  
- % Identity 91.6  
- Alignment Length 137  
- Location of Alignment in SEQ ID NO 2072: from 2 to 127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2073  
- Ceres seq\_id 1502077

- Location of start within SEQ ID NO 2070: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13938
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2073: from 43 to 93 aa.
  
- Alignment No. 13939
- Mucin-like glycoprotein
- Location within SEQ ID NO 2073: from 7 to 126 aa.
  
- Alignment No. 13940
- Mucin-like glycoprotein
- Location within SEQ ID NO 2073: from 31 to 121 aa.
  
- Alignment No. 13941
- Mucin-like glycoprotein
- Location within SEQ ID NO 2073: from 31 to 124 aa.
  
- Alignment No. 13942
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 14 to 126 aa.
  
- Alignment No. 13943
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 21 to 126 aa.
  
- Alignment No. 13944
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 32 to 107 aa.
  
- Alignment No. 13945
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 89 aa.
  
- Alignment No. 13946
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 113 aa.
  
- Alignment No. 13947
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 120 aa.
  
- Alignment No. 13948
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 123 aa.
  
- Alignment No. 13949
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2073: from 34 to 126 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13950
- gi No. 100687
- % Identity 70.6
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2073: from 5 to 126
  
- Alignment No. 13951
- gi No. 228937

- % Identity 91.5  
- Alignment Length 136  
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13952  
- gi No. 228938  
- % Identity 93.3  
- Alignment Length 134  
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13953  
- gi No. 283032  
- % Identity 96.2  
- Alignment Length 130  
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13954  
- gi No. 283045  
- % Identity 91.9  
- Alignment Length 136  
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

- Alignment No. 13955  
- gi No. 458468  
- % Identity 71.8  
- Alignment Length 39  
- Location of Alignment in SEQ ID NO 2073: from 80 to 114

- Alignment No. 13956  
- gi No. 458468  
- % Identity 75.7  
- Alignment Length 39  
- Location of Alignment in SEQ ID NO 2073: from 91 to 126

- Alignment No. 13957  
- gi No. 458468  
- % Identity 76.3  
- Alignment Length 40  
- Location of Alignment in SEQ ID NO 2073: from 85 to 122

- Alignment No. 13958  
- gi No. 458468  
- % Identity 75  
- Alignment Length 43  
- Location of Alignment in SEQ ID NO 2073: from 85 to 124

- Alignment No. 13959  
- gi No. 458468  
- % Identity 72.5  
- Alignment Length 43  
- Location of Alignment in SEQ ID NO 2073: from 85 to 124

- Alignment No. 13960  
- gi No. 458468  
- % Identity 71.4  
- Alignment Length 44  
- Location of Alignment in SEQ ID NO 2073: from 80 to 121

- Alignment No. 13961  
- gi No. 82698  
- % Identity 91.6

- Alignment Length 137
- Location of Alignment in SEQ ID NO 2073: from 1 to 126

Maximum Length Sequence corresponding to clone ID 300006

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2074
- Ceres seq\_id 1502086

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2075
- Ceres seq\_id 1502087
- Location of start within SEQ ID NO 2074: at 222 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13962
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2075: from 35 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13963
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112
- Alignment No. 13964
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112
- Alignment No. 13965
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112
- Alignment No. 13966
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2075: from 3 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2076
- Ceres seq\_id 1502088
- Location of start within SEQ ID NO 2074: at 294 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13967
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2076: from 11 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13968
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

- Alignment No. 13969
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88
- Alignment No. 13970
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88
- Alignment No. 13971
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2076: from 1 to 88

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2077
- Ceres seq\_id 1502089
- Location of start within SEQ ID NO 2074: at 312 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13972
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2077: from 5 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13973
- gi No. 3850816
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82
- Alignment No. 13974
- gi No. 3850818
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82
- Alignment No. 13975
- gi No. 3850819
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82
- Alignment No. 13976
- gi No. 5668775
- % Identity 78.2
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2077: from 1 to 82

Maximum Length Sequence corresponding to clone ID 300011

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2078
- Ceres seq\_id 1502090

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2079
- Ceres seq\_id 1502091

- Location of start within SEQ ID NO 2078: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13977
- gi No. 2134207
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92

- Alignment No. 13978
- gi No. 2134208
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92

- Alignment No. 13979
- gi No. 2134209
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92

- Alignment No. 13980
- gi No. 2134210
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2079: from 71 to 92

- Alignment No. 13981
- gi No. 2134211
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2079: from 71 to 92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2080
- Ceres seq\_id 1502092
- Location Of start within SEQ ID NO 2078: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2081
- Ceres seq\_id 1502093
- Location of start within SEQ ID NO 2078: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300014

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2082
- Ceres seq\_id 1502094

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2083
- Ceres seq\_id 1502095
- Location of start within SEQ ID NO 2082: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13982
- Glutathione S-transferases.
- Location within SEQ ID NO 2083: from 32 to 211 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2084
- Ceres seq\_id 1502096
- Location of start within SEQ ID NO 2082: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13983
- Glutathione S-transferases.
- Location within SEQ ID NO 2084: from 26 to 205 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2085
- Ceres seq\_id 1502097
- Location of start within SEQ ID NO 2082: at 50 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13984
- Glutathione S-transferases.
- Location within SEQ ID NO 2085: from 16 to 195 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 300700

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2086
- Ceres seq\_id 1502100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2087
- Ceres seq\_id 1502101
- Location of start within SEQ ID NO 2086: at 53 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2088
- Ceres seq\_id 1502102
- Location of start within SEQ ID NO 2086: at 171 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13985
- Pentapeptide repeats (8 copies)
- Location within SEQ ID NO 2088: from 101 to 135 aa.

(D) Related Amino Acid Sequences



Maximum Length Sequence corresponding to clone ID 302706

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2089
- Ceres seq\_id 1502130

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2090
- Ceres seq\_id 1502131
- Location of start within SEQ ID NO 2089: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13986
- gi No. 1352442
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155
- Alignment No. 13987
- gi No. 170753
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155
- Alignment No. 13988
- gi No. 3342823
- % Identity 84.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2090: from 58 to 155
- Alignment No. 13989
- gi No. 547713
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2090: from 55 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2091
- Ceres seq\_id 1502132
- Location of start within SEQ ID NO 2089: at 163 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 13990
- gi No. 1352442
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101
- Alignment No. 13991
- gi No. 170753
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101
- Alignment No. 13992
- gi No. 3342823
- % Identity 84.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2091: from 4 to 101

- Alignment No. 13993
- gi No. 547713
- % Identity 79.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2091: from 1 to 101

Maximum Length Sequence corresponding to clone ID 302718

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2092
- Ceres seq\_id 1502133

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2093
- Ceres seq\_id 1502134
- Location of start within SEQ ID NO 2092: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2094
- Ceres seq\_id 1502135
- Location of start within SEQ ID NO 2092: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13994
- Protamine P1
- Location within SEQ ID NO 2094: from 22 to 94 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2095
- Ceres seq\_id 1502136
- Location of start within SEQ ID NO 2092: at 247 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13995
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2095: from 23 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13996
- gi No. 266410
- % Identity 82.9
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2095: from 7 to 83

Maximum Length Sequence corresponding to clone ID 302744

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2096
- Ceres seq\_id 1502153

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2097
- Ceres seq\_id 1502154
- Location of start within SEQ ID NO 2096: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 13997
- Cytochrome P450
- Location within SEQ ID NO 2097: from 66 to 173 aa.

(D) Related Amino Acid Sequences

- Alignment No. 13998
- gi No. 1870203
- % Identity 99.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 2097: from 10 to 173
- Alignment No. 13999
- gi No. 5420116
- % Identity 99.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 2097: from 11 to 173

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2098
- Ceres seq\_id 1502155
- Location of start within SEQ ID NO 2096: at 28 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14000
- Cytochrome P450
- Location within SEQ ID NO 2098: from 57 to 164 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14001
- gi No. 1870203
- % Identity 99.4
- Alignment Length 165
- Location of Alignment in SEQ ID NO 2098: from 1 to 164
- Alignment No. 14002
- gi No. 5420116
- % Identity 99.4
- Alignment Length 164
- Location of Alignment in SEQ ID NO 2098: from 2 to 164

Maximum Length Sequence corresponding to clone ID 303152

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2099
- Ceres seq\_id 1502165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2100
- Ceres seq\_id 1502166
- Location of start within SEQ ID NO 2099: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2101
- Ceres seq\_id 1502167
- Location of start within SEQ ID NO 2099: at 177 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14003
- RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
- Location within SEQ ID NO 2101: from 60 to 126 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 303165

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2102
- Ceres seq\_id 1502168

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2103
- Ceres seq\_id 1502169
- Location of start within SEQ ID NO 2102: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14004
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 2103: from 18 to 153 aa.
- Alignment No. 14005
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 2103: from 21 to 140 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14006
- gi No. 3269286
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2103: from 19 to 52
- Alignment No. 14007
- gi No. 553035
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2103: from 20 to 50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2104
- Ceres seq\_id 1502170
- Location of start within SEQ ID NO 2102: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14008
- 3-beta hydroxysteroid dehydrogenase/isomerase family
- Location within SEQ ID NO 2104: from 5 to 140 aa.
- Alignment No. 14009
- NAD dependent epimerase/dehydratase family
- Location within SEQ ID NO 2104: from 8 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14010
- gi No. 3269286
- % Identity 70.6
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2104: from 6 to 39

- Alignment No. 14011
- gi No. 553035
- % Identity 74.2
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2104: from 7 to 37

Maximum Length Sequence corresponding to clone ID 303456

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2105
- Ceres seq\_id 1502189

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2106
- Ceres seq\_id 1502190
- Location of start within SEQ ID NO 2105: at 192 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14012
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2106: from 14 to 165 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14013
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2106: from 14 to 165

- Alignment No. 14014
- gi No. 2529670
- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2106: from 14 to 165

- Alignment No. 14015
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2106: from 14 to 165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2107
- Ceres seq\_id 1502191
- Location of start within SEQ ID NO 2105: at 285 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14016
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2107: from 1 to 134 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14017
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2107: from 1 to 134

- Alignment No. 14018
- gi No. 2529670

- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2107: from 1 to 134
- Alignment No. 14019
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2107: from 1 to 134

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2108
- Ceres seq\_id 1502192
- Location of start within SEQ ID NO 2105: at 315 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14020
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2108: from 1 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14021
- gi No. 1172977
- % Identity 80.9
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2108: from 1 to 124
- Alignment No. 14022
- gi No. 2529670
- % Identity 76.5
- Alignment Length 153
- Location of Alignment in SEQ ID NO 2108: from 1 to 124
- Alignment No. 14023
- gi No. 3021348
- % Identity 80.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2108: from 1 to 124

Maximum Length Sequence corresponding to clone ID 303464

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2109
- Ceres seq\_id 1502193

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2110
- Ceres seq\_id 1502194
- Location of start within SEQ ID NO 2109: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14024
- gi No. 100219
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2110: from 7 to 24
- Alignment No. 14025
- gi No. 100219
- % Identity 73.7

- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25
- Alignment No. 14026
- gi No. 100219
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2110: from 7 to 25

Maximum Length Sequence corresponding to clone ID 303902

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2111
- Ceres seq\_id 1502205

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2112
- Ceres seq\_id 1502206
- Location of start within SEQ ID NO 2111: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14027
- Glutathione peroxidases
- Location within SEQ ID NO 2112: from 9 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14028
- gi No. 1362150
- % Identity 87
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2112: from 53 to 98
- Alignment No. 14029
- gi No. 1708062
- % Identity 71.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14030
- gi No. 2274857
- % Identity 71.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14031
- gi No. 232190
- % Identity 74.7
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2112: from 1 to 98
- Alignment No. 14032
- gi No. 2388885
- % Identity 76.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2112: from 4 to 98
- Alignment No. 14033
- gi No. 2388887
- % Identity 72.4
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2112: from 70 to 98

- Alignment No. 14034  
- gi No. 2392021  
- % Identity 75  
- Alignment Length 100  
- Location of Alignment in SEQ ID NO 2112: from 1 to 98

- Alignment No. 14035  
- gi No. 2632109  
- % Identity 71.1  
- Alignment Length 90  
- Location of Alignment in SEQ ID NO 2112: from 9 to 98

- Alignment No. 14036  
- gi No. 2746232  
- % Identity 74  
- Alignment Length 100  
- Location of Alignment in SEQ ID NO 2112: from 1 to 98

- Alignment No. 14037  
- gi No. 2760606  
- % Identity 86.7  
- Alignment Length 98  
- Location of Alignment in SEQ ID NO 2112: from 1 to 98

- Alignment No. 14038  
- gi No. 3023912  
- % Identity 94.1  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2112: from 59 to 75

- Alignment No. 14039  
- gi No. 3913793  
- % Identity 81.4  
- Alignment Length 86  
- Location of Alignment in SEQ ID NO 2112: from 13 to 98

- Alignment No. 14040  
- gi No. 3913794  
- % Identity 71.4  
- Alignment Length 98  
- Location of Alignment in SEQ ID NO 2112: from 1 to 98

- Alignment No. 14041  
- gi No. 4138608  
- % Identity 91.7  
- Alignment Length 72  
- Location of Alignment in SEQ ID NO 2112: from 1 to 72

- Alignment No. 14042  
- gi No. 4584526  
- % Identity 73.7  
- Alignment Length 99  
- Location of Alignment in SEQ ID NO 2112: from 1 to 98

- Alignment No. 14043  
- gi No. 485512  
- % Identity 79.2  
- Alignment Length 96  
- Location of Alignment in SEQ ID NO 2112: from 3 to 98

- Alignment No. 14044

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2084  
2085  
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2088  
2089  
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2097  
2098  
2099  
2100  
2101  
2102  
2103  
2104  
2105  
2106  
2107  
2108  
210



- gi No. 544437
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2112: from 3 to 98

Maximum Length Sequence corresponding to clone ID 304670

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2113
- Ceres seq\_id 1502220

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2114
- Ceres seq\_id 1502221
- Location of start within SEQ ID NO 2113: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14045
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14046
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2114: from 95 to 173
  
- Alignment No. 14047
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14048
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14049
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14050
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14051
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2114: from 94 to 173
  
- Alignment No. 14052
- gi No. 687927

- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2114: from 106 to 125

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2115
- Ceres seq\_id 1502222
- Location of start within SEQ ID NO 2113: at 11 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14053
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14054
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2115: from 92 to 170
  
- Alignment No. 14055
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14056
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14057
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14058
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14059
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2115: from 91 to 170
  
- Alignment No. 14060
- gi No. 687927
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2115: from 103 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2116
- Ceres seq\_id 1502223
- Location of start within SEQ ID NO 2116: at 173 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14061
- gi No. 1172637
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14062
- gi No. 1172638
- % Identity 75
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2116: from 38 to 116
- Alignment No. 14063
- gi No. 1709797
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14064
- gi No. 2492517
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14065
- gi No. 263099
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14066
- gi No. 2791680
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14067
- gi No. 3450955
- % Identity 70.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2116: from 37 to 116
- Alignment No. 14068
- gi No. 687927
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2116: from 49 to 68

Maximum Length Sequence corresponding to clone ID 304673

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2117
- Ceres seq\_id 1502224

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2118

- Ceres seq\_id 1502225
- Location of start within SEQ ID NO 2117: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14069
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2118: from 110 to 183 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2119
- Ceres seq\_id 1502226
- Location of start within SEQ ID NO 2117: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14070
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2119: from 96 to 169 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2120
- Ceres seq\_id 1502227
- Location of start within SEQ ID NO 2117: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14071
- Acetyltransferase (GNAT) family
- Location within SEQ ID NO 2120: from 75 to 148 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 304677

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2121
- Ceres seq\_id 1502228

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2122
- Ceres seq\_id 1502229
- Location of start within SEQ ID NO 2121: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2123
- Ceres seq\_id 1502230
- Location of start within SEQ ID NO 2121: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14072
- Pollen allergen
- Location within SEQ ID NO 2123: from 28 to 105 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2124
- Ceres seq\_id 1502231
- Location of start within SEQ ID NO 2121: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14073
- Pollen allergen
- Location within SEQ ID NO 2124: from 16 to 93 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311105

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2125
- Ceres seq\_id 1502270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2126
- Ceres seq\_id 1502271
- Location of start within SEQ ID NO 2125: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14074
- Ras family
- Location within SEQ ID NO 2126: from 31 to 158 aa.
- Alignment No. 14075
- ADP-ribosylation factor family
- Location within SEQ ID NO 2126: from 31 to 148 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14076
- gi No. 1370172
- % Identity 72.9
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2126: from 20 to 158
- Alignment No. 14077
- gi No. 2723477
- % Identity 75.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2126: from 19 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2127
- Ceres seq\_id 1502272
- Location of start within SEQ ID NO 2125: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14078
- Ras family
- Location within SEQ ID NO 2127: from 14 to 141 aa.
- Alignment No. 14079
- ADP-ribosylation factor family
- Location within SEQ ID NO 2127: from 14 to 131 aa.

- (D) Related Amino Acid Sequences
  - Alignment No. 14080
  - gi No. 1370172
  - % Identity 72.9
  - Alignment Length 140
  - Location of Alignment in SEQ ID NO 2127: from 3 to 141
- Alignment No. 14081
- gi No. 2723477
- % Identity 75.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2127: from 2 to 141

Maximum Length Sequence corresponding to clone ID 311199

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2128
- Ceres seq\_id 1502285

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2129
- Ceres seq\_id 1502286
- Location of start within SEQ ID NO 2128: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14082
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2129: from 94 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2130
- Ceres seq\_id 1502287
- Location of start within SEQ ID NO 2128: at 54 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14083
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2130: from 77 to 95

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2131
- Ceres seq\_id 1502288
- Location of start within SEQ ID NO 2128: at 66 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14084
- gi No. 1002380
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2131: from 73 to 91

Maximum Length Sequence corresponding to clone ID 311212

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2132  
- Ceres seq\_id 1502297  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2133  
- Ceres seq\_id 1502298  
- Location of start within SEQ ID NO 2132: at 2 nt.  
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2134  
- Ceres seq\_id 1502299  
- Location of start within SEQ ID NO 2132: at 3 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences  
- Alignment No. 14085  
- gi No. 102706  
- % Identity 75  
- Alignment Length 16  
- Location of Alignment in SEQ ID NO 2134: from 81 to 96

- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2135  
- Ceres seq\_id 1502300  
- Location of start within SEQ ID NO 2132: at 48 nt.

- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences  
- Alignment No. 14086  
- gi No. 102706  
- % Identity 75  
- Alignment Length 16  
- Location of Alignment in SEQ ID NO 2135: from 66 to 81

Maximum Length Sequence corresponding to clone ID 311293

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2136  
- Ceres seq\_id 1502315  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2137  
- Ceres seq\_id 1502316  
- Location of start within SEQ ID NO 2136: at 63 nt.  
(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
(D) Related Amino Acid Sequences  
- Alignment No. 14087  
- gi No. 2739368  
- % Identity 71.1  
- Alignment Length 76  
- Location of Alignment in SEQ ID NO 2137: from 56 to 130  
(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2138  
- Ceres seq\_id 1502317

- Location of start within SEQ ID NO 2136: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14088
- gi No. 2739368
- % Identity 71.1
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2138: from 1 to 75

Maximum Length Sequence corresponding to clone ID 311422

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2139
- Ceres seq\_id 1502363

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2140
- Ceres seq\_id 1502364
- Location of start within SEQ ID NO 2139: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14089
- gi No. 396749
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2140: from 84 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2141
- Ceres seq\_id 1502365
- Location of start within SEQ ID NO 2139: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2142
- Ceres seq\_id 1502366
- Location of start within SEQ ID NO 2139: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14090
- gi No. 2828285
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2142: from 138 to 157
- Alignment No. 14091
- gi No. 2832638
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2142: from 138 to 157

Maximum Length Sequence corresponding to clone ID 311431

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2143



- Ceres seq\_id 1502367
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2144
  - Ceres seq\_id 1502368
  - Location of start within SEQ ID NO 2143: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14092
- Kinesin motor domain
- Location within SEQ ID NO 2144: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14093
- gi No. 1170619
- % Identity 89.7
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78
  
- Alignment No. 14094
- gi No. 1170620
- % Identity 88.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78
  
- Alignment No. 14095
- gi No. 1170621
- % Identity 87.2
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78
  
- Alignment No. 14096
- gi No. 125477
- % Identity 70.9
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2144: from 1 to 77
  
- Alignment No. 14097
- gi No. 2826849
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15
  
- Alignment No. 14098
- gi No. 3023586
- % Identity 70.1
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2144: from 1 to 77
  
- Alignment No. 14099
- gi No. 3913957
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15
  
- Alignment No. 14100
- gi No. 4490714
- % Identity 88.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2144: from 1 to 78

- Alignment No. 14101
- gi No. 4504869
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2144: from 1 to 15

Maximum Length Sequence corresponding to clone ID 311460

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2145
- Ceres seq\_id 1502373

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2146
- Ceres seq\_id 1502374
- Location of start within SEQ ID NO 2145: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2147
- Ceres seq\_id 1502375
- Location of start within SEQ ID NO 2145: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14102
- gi No. 2655291
- % Identity 82.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2147: from 1 to 66
- Alignment No. 14103
- gi No. 2979494
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2147: from 22 to 58

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2148
- Ceres seq\_id 1502376
- Location of start within SEQ ID NO 2145: at 272 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14104
- gi No. 2655291
- % Identity 82.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2148: from 1 to 38
- Alignment No. 14105
- gi No. 2979494
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2148: from 1 to 30

Maximum Length Sequence corresponding to clone ID 311474

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2149

- Ceres seq\_id 1502381

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2150

- Ceres seq\_id 1502382

- Location of start within SEQ ID NO 2149: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14106

- Eukaryotic protein kinase domain

- Location within SEQ ID NO 2150: from 1 to 131 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14107

- gi No. 1066501

- % Identity 70.2

- Alignment Length 132

- Location of Alignment in SEQ ID NO 2150: from 3 to 131

- Alignment No. 14108

- gi No. 1168470

- % Identity 73.9

- Alignment Length 135

- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14109

- gi No. 1168471

- % Identity 77.4

- Alignment Length 94

- Location of Alignment in SEQ ID NO 2150: from 42 to 131

- Alignment No. 14110

- gi No. 1778444

- % Identity 75.6

- Alignment Length 45

- Location of Alignment in SEQ ID NO 2150: from 88 to 131

- Alignment No. 14111

- gi No. 2852447

- % Identity 72

- Alignment Length 133

- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14112

- gi No. 2852449

- % Identity 71.2

- Alignment Length 133

- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14113

- gi No. 3075390

- % Identity 76.2

- Alignment Length 131

- Location of Alignment in SEQ ID NO 2150: from 3 to 131

- Alignment No. 14114

- gi No. 3461835

- % Identity 73.1

- Alignment Length 135

- Location of Alignment in SEQ ID NO 2150: from 1 to 131

- Alignment No. 14115
- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
- Alignment No. 14116
- gi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
- Alignment No. 14117
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2150: from 42 to 131
- Alignment No. 14118
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2150: from 3 to 131
- Alignment No. 14119
- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2150: from 69 to 130
- Alignment No. 14120
- gi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2150: from 1 to 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2151
- Ceres seq\_id 1502383
- Location of start within SEQ ID NO 2149: at 160 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14121
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2151: from 1 to 78 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14122
- gi No. 1066501
- % Identity 70.2
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14123
- gi No. 1168470
- % Identity 73.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

- Alignment No. 14124
- gi No. 1168471
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14125
- gi No. 1778444
- % Identity 75.6
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2151: from 35 to 78
- Alignment No. 14126
- gi No. 2852447
- % Identity 72
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14127
- gi No. 2852449
- % Identity 71.2
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14128
- gi No. 3075390
- % Identity 76.2
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14129
- gi No. 3461835
- % Identity 73.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14130
- gi No. 3805765
- % Identity 70.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14131
- gi No. 4006829
- % Identity 74.6
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14132
- gi No. 4432889
- % Identity 77.4
- Alignment Length 94
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14133
- gi No. 4585873
- % Identity 73.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2151: from 1 to 78
- Alignment No. 14134

- gi No. 4753653
- % Identity 71
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2151: from 16 to 77
- Alignment No. 14135
- gi No. 5091529
- % Identity 83.3
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2151: from 1 to 78

Maximum Length Sequence corresponding to clone ID 311490

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2152
- Ceres seq\_id 1502387

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2153
- Ceres seq\_id 1502388
- Location of start within SEQ ID NO 2152: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14136
- Ribosomal protein L5
- Location within SEQ ID NO 2153: from 65 to 100 aa.
- Alignment No. 14137
- ribosomal L5P family C-terminus
- Location within SEQ ID NO 2153: from 104 to 158 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14138
- gi No. 1125808
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14139
- gi No. 1172816
- % Identity 96.8
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14140
- gi No. 1172817
- % Identity 97.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14141
- gi No. 1172952
- % Identity 84.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158
- Alignment No. 14142
- gi No. 1172954
- % Identity 78.9
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14143  
- gi No. 1172969  
- % Identity 97.9  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14144  
- gi No. 1173055  
- % Identity 100  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14145  
- gi No. 1246369  
- % Identity 74.5  
- Alignment Length 94  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14146  
- gi No. 132649  
- % Identity 85.3  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14147  
- gi No. 132777  
- % Identity 74.7  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14148  
- gi No. 132951  
- % Identity 83.2  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14149  
- gi No. 132992  
- % Identity 77.8  
- Alignment Length 63  
- Location of Alignment in SEQ ID NO 2153: from 65 to 127

- Alignment No. 14150  
- gi No. 1350658  
- % Identity 83.2  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14151  
- gi No. 1350659  
- % Identity 77.9  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14152  
- gi No. 1710480  
- % Identity 75.8  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14153

- gi No. 1710494  
- % Identity 87.4  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14154  
- gi No. 2500240  
- % Identity 84  
- Alignment Length 94  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14155  
- gi No. 2500241  
- % Identity 81.3  
- Alignment Length 91  
- Location of Alignment in SEQ ID NO 2153: from 65 to 155

- Alignment No. 14156  
- gi No. 2570507  
- % Identity 89.5  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14157  
- gi No. 3914659  
- % Identity 84.2  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14158  
- gi No. 4322  
- % Identity 82.1  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14159  
- gi No. 4432750  
- % Identity 96  
- Alignment Length 25  
- Location of Alignment in SEQ ID NO 2153: from 65 to 89

- Alignment No. 14160  
- gi No. 4506595  
- % Identity 81.1  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14161  
- gi No. 4512679  
- % Identity 88.6  
- Alignment Length 105  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14162  
- gi No. 4586222  
- % Identity 85.3  
- Alignment Length 95  
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

- Alignment No. 14163  
- gi No. 71107



- % Identity 83.2
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2153: from 65 to 158

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2154
- Ceres seq\_id 1502389
- Location of start within SEQ ID NO 2152: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14164
- gi No. 1172816
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

- Alignment No. 14165
- gi No. 1172817
- % Identity 85.2
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2154: from 2 to 28

- Alignment No. 14166
- gi No. 1172969
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

- Alignment No. 14167
- gi No. 1173055
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

- Alignment No. 14168
- gi No. 2570507
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2154: from 1 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2155
- Ceres seq\_id 1502390
- Location of start within SEQ ID NO 2152: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14169
- gi No. 1172816
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

- Alignment No. 14170
- gi No. 1172817
- % Identity 85.2
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

- Alignment No. 14171
- gi No. 1172969
- % Identity 85.7
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18
  
- Alignment No. 14172
- gi No. 1173055
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18
  
- Alignment No. 14173
- gi No. 2570507
- % Identity 89.3
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2155: from 1 to 18

Maximum Length Sequence corresponding to clone ID 311538

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2156
- Ceres seq\_id 1502407

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2157
- Ceres seq\_id 1502408
- Location of start within SEQ ID NO 2156: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14174
- Peroxidase
- Location within SEQ ID NO 2157: from 61 to 134 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2158
- Ceres seq\_id 1502409
- Location of start within SEQ ID NO 2156: at 210 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14175
- Peroxidase
- Location within SEQ ID NO 2158: from 15 to 88 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311554

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2159
- Ceres seq\_id 1502420

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2160
- Ceres seq\_id 1502421
- Location of start within SEQ ID NO 2159: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14176

- Ribosomal protein S12
- Location within SEQ ID NO 2160: from 58 to 144 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14177
- gi No. 1173187
- % Identity 97.7
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14178
- gi No. 1350965
- % Identity 97.7
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2160: from 58 to 143
- Alignment No. 14179
- gi No. 1850766
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14180
- gi No. 2500455
- % Identity 74.2
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14181
- gi No. 2829742
- % Identity 81.8
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14182
- gi No. 2833303
- % Identity 79.5
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144
- Alignment No. 14183
- gi No. 3088342
- % Identity 92.9
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2160: from 118 to 144
- Alignment No. 14184
- gi No. 417716
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2160: from 58 to 144
- Alignment No. 14185
- gi No. 4493905
- % Identity 75.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2160: from 54 to 144
- Alignment No. 14186
- gi No. 4506701
- % Identity 81.8

- Alignment Length 88
- Location of Alignment in SEQ ID NO 2160: from 59 to 144

Maximum Length Sequence corresponding to clone ID 311571

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2161
- Ceres seq\_id 1502422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2162
- Ceres seq\_id 1502423
- Location of start within SEQ ID NO 2161: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14187
- AhpC/TSA family
- Location within SEQ ID NO 2162: from 11 to 67 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14188
- gi No. 5441879
- % Identity 80
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2162: from 28 to 67

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2163
- Ceres seq\_id 1502424
- Location of start within SEQ ID NO 2161: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14189
- AhpC/TSA family
- Location within SEQ ID NO 2163: from 66 to 142 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14190
- gi No. 5441879
- % Identity 72.2
- Alignment Length 97
- Location of Alignment in SEQ ID NO 2163: from 65 to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2164
- Ceres seq\_id 1502425
- Location of start within SEQ ID NO 2161: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311596

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2165
- Ceres seq\_id 1502429

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2166
- Ceres seq\_id 1502430
- Location of start within SEQ ID NO 2165: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14191
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2166: from 1 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2167
- Ceres seq\_id 1502431
- Location of start within SEQ ID NO 2165: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14192
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2167: from 1 to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2168
- Ceres seq\_id 1502432
- Location of start within SEQ ID NO 2165: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14193
- gi No. 417298
- % Identity 74.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2168: from 1 to 68

Maximum Length Sequence corresponding to clone ID 311614

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2169
- Ceres seq\_id 1502441

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2170
- Ceres seq\_id 1502442
- Location of start within SEQ ID NO 2169: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14194
- gi No. 3335351
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2170: from 41 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2171
- Ceres seq\_id 1502443
- Location of start within SEQ ID NO 2169: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 14195
  - gi No. 2924785
  - % Identity 72.2
  - Alignment Length 18
  - Location of Alignment in SEQ ID NO 2171: from 12 to 29

Maximum Length Sequence corresponding to clone ID 311726

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2172
- Ceres seq\_id 1502461

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2173
- Ceres seq\_id 1502462
- Location of start within SEQ ID NO 2172: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 14196
  - gi No. 4028260
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2173: from 38 to 48

Maximum Length Sequence corresponding to clone ID 311791

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2174
- Ceres seq\_id 1502479

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2175
- Ceres seq\_id 1502480
- Location of start within SEQ ID NO 2174: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2176
- Ceres seq\_id 1502481
- Location of start within SEQ ID NO 2174: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14197
- Elongation factor 1 gamma, conserved domain.
- Location within SEQ ID NO 2176: from 29 to 81 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14198
  - gi No. 2160158
  - % Identity 75.9
  - Alignment Length 79
  - Location of Alignment in SEQ ID NO 2176: from 1 to 73
- 
- Alignment No. 14199
  - gi No. 3868758
  - % Identity 87.8

- Alignment Length 74  
- Location of Alignment in SEQ ID NO 2176: from 1 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2177
- Ceres seq\_id 1502482
- Location of start within SEQ ID NO 2174: at 7 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 311814

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2178
- Ceres seq id 1502487

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2179
- Ceres seq\_id 1502488
- Location of start within SEQ ID NO 2178: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14200
- G-protein alpha subunit
- Location within SEQ ID NO 2179: from 46 to 112 aa.

- Alignment No. 14201
- ADP-ribosylation factor family
- Location within SEQ ID NO 2179: from 1 to 117 aa.

- Alignment No. 14202
- Ras family
- Location within SEO ID NO 2179: from 18 to 92 aa.

#### (D) Related Amino Acid Sequences

- ```
- Alignment No. 14203
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEO ID NO 2179: from 1 to 117
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(B) Polypeptide Sequence

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- Pat. Appln. SEQ ID NO 2180
- Ceres seq_id 1502489
- Location of start within SEQ ID NO 2178: at 150 nt.
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(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14204
- G-protein alpha subunit
- Location within SEQ ID NO 2180: from 30 to 96 aa.

- Alignment No. 14205
- ADP-ribosylation factor family
- Location within SEQ ID NO 2180: from 1 to 101 aa.

- Alignment No. 14206
- Ras family
- Location within SEQ ID NO 2180: from 2 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14207
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2180: from 1 to 101

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2181
- Ceres seq\_id 1502490
- Location of start within SEQ ID NO 2178: at 162 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14208
- G-protein alpha subunit
- Location within SEQ ID NO 2181: from 26 to 92 aa.
- Alignment No. 14209
- ADP-ribosylation factor family
- Location within SEQ ID NO 2181: from 1 to 97 aa.
- Alignment No. 14210
- Ras family
- Location within SEQ ID NO 2181: from 1 to 72 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14211
- gi No. 4309728
- % Identity 91.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2181: from 1 to 97

Maximum Length Sequence corresponding to clone ID 311865

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2182
- Ceres seq\_id 1502514

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2183
- Ceres seq\_id 1502515
- Location of start within SEQ ID NO 2182: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2184
- Ceres seq\_id 1502516
- Location of start within SEQ ID NO 2182: at 89 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14212
- Ribosomal L29 protein
- Location within SEQ ID NO 2184: from 6 to 69 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14213
- gi No. 3355468
- % Identity 85.2



- Alignment Length 122
- Location of Alignment in SEQ ID NO 2184: from 1 to 122

Maximum Length Sequence corresponding to clone ID 311870

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2185
- Ceres seq\_id 1502517

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2186
- Ceres seq\_id 1502518
- Location of start within SEQ ID NO 2185: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14214
- Protein-tyrosine phosphatase
- Location within SEQ ID NO 2186: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14215
- gi No. 3413473
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2186: from 1 to 60
- Alignment No. 14216
- gi No. 3413500
- % Identity 73.3
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2186: from 1 to 60
- Alignment No. 14217
- gi No. 348540
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2186: from 1 to 14
- Alignment No. 14218
- gi No. 464498
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2186: from 1 to 14

Maximum Length Sequence corresponding to clone ID 311889

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2187
- Ceres seq\_id 1502519

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2188
- Ceres seq\_id 1502520
- Location of start within SEQ ID NO 2187: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2189
- Ceres seq\_id 1502521
- Location of start within SEQ ID NO 2187: at 197 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14219
- gi No. 1769895
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2189: from 1 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2190
- Ceres seq\_id 1502522
- Location of start within SEQ ID NO 2187: at 218 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14220
- gi No. 1769895
- % Identity 72.4
- Alignment Length 76
- Location of Alignment in SEQ ID NO 2190: from 1 to 69

Maximum Length Sequence corresponding to clone ID 311911

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2191
- Ceres seq\_id 1502527

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2192
- Ceres seq\_id 1502528
- Location of start within SEQ ID NO 2191: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14221
- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 2192: from 1 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14222
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14223
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14224
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

- Alignment No. 14225
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14226
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14227
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14228
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2192: from 1 to 91
- Alignment No. 14229
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14230
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14231
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14232
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14233
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14234
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14235
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

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- Alignment No. 14236
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14237
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14238
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96
- Alignment No. 14239
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2192: from 1 to 96

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2193
- Ceres seq\_id 1502529
- Location of start within SEQ ID NO 2191: at 76 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14240
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14241
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14242
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14243
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14244
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96

- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14245
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14246
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2193: from 1 to 66
- Alignment No. 14247
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14248
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14249
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14250
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14251
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14252
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14253
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71
- Alignment No. 14254
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

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- Alignment No. 14255
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

- Alignment No. 14256
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

- Alignment No. 14257
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2193: from 1 to 71

```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2194
- Ceres seq\_id 1502530
- Location of start within SEQ ID NO 2191: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

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Alignment No. 14258
- gi No. 1078797
- % Identity 80.2
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Alignment No. 14259
- gi No. 1170767
- % Identity 75
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Alignment No. 14260
- gi No. 1262435
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Alignment No. 14261
- gi No. 1346812
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Alignment No. 14262
- gi No. 1709799
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Alignment No. 14263
- gi No. 1709800
- % Identity 81.3
- Alignment Length 96

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- Location of Alignment in SEQ ID NO 2194: from 1 to 63
- Alignment No. 14264
- gi No. 228885
- % Identity 70.3
- Alignment Length 91
- Location of Alignment in SEQ ID NO 2194: from 1 to 63

- Alignment No. 14265
- gi No. 2492521
- % Identity 76
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14266
- gi No. 2564007
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14267
- gi No. 2661071
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14268
- gi No. 2815905
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14269
- gi No. 2982331
- % Identity 94.8
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14270
- gi No. 3041724
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14271
- gi No. 3122626
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14272
- gi No. 3790757
- % Identity 77.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

- Alignment No. 14273
- gi No. 3979998
- % Identity 78.1
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
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- Alignment No. 14274
- gi No. 4506213
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68
- Alignment No. 14275
- gi No. 464863
- % Identity 81.3
- Alignment Length 96
- Location of Alignment in SEQ ID NO 2194: from 1 to 68

Maximum Length Sequence corresponding to clone ID 311937

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2195
- Ceres seq\_id 1502542

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2196
- Ceres seq\_id 1502543
- Location of start within SEQ ID NO 2195: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14276
- Ras family
- Location within SEQ ID NO 2196: from 69 to 147 aa.
- Alignment No. 14277
- ADP-ribosylation factor family
- Location within SEQ ID NO 2196: from 52 to 169 aa.
- Alignment No. 14278
- G-protein alpha subunit
- Location within SEQ ID NO 2196: from 94 to 169 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14279
- gi No. 1065361
- % Identity 90.8
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 52 to 169
- Alignment No. 14280
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14281
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14282
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169



- Alignment No. 14283  
- gi No. 114128  
- % Identity 74.8  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2196: from 56 to 169

- Alignment No. 14284  
- gi No. 114131  
- % Identity 74.4  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14285  
- gi No. 1168489  
- % Identity 85  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14286  
- gi No. 1351973  
- % Identity 86.7  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14287  
- gi No. 1351974  
- % Identity 97.5  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14288  
- gi No. 1703373  
- % Identity 90.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14289  
- gi No. 1703374  
- % Identity 95.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14290  
- gi No. 1703375  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14291  
- gi No. 1703376  
- % Identity 93.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14292  
- gi No. 1703377  
- % Identity 90.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14293

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- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14294
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14295
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14296
- gi No. 2129946
- % Identity 97.7
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2196: from 51 to 137
- Alignment No. 14297
- gi No. 2293566
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14298
- gi No. 2462736
- % Identity 97.6
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2196: from 51 to 92
- Alignment No. 14299
- gi No. 2492925
- % Identity 80
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14300
- gi No. 2689631
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14301
- gi No. 283391
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14302
- gi No. 2852443
- % Identity 95
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14303
- gi No. 2854182

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- % Identity 87.4
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14304
- gi No. 3182915
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14305
- gi No. 3182916
- % Identity 80.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14306
- gi No. 3182917
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14307
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14308
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2196: from 68 to 160

- Alignment No. 14309
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169

- Alignment No. 14310
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2196: from 69 to 169

- Alignment No. 14311
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

- Alignment No. 14312
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2196: from 51 to 116

- Alignment No. 14313
- gi No. 4324967
- % Identity 98.3
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- Alignment Length 117
- Location of Alignment in SEQ ID NO 2196: from 54 to 169
- Alignment No. 14314
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14315
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14316
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14317
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14318
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14319
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14320
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14321
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14322
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14323
- gi No. 543842
- % Identity 90
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14324
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14325
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14326
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2196: from 48 to 169
- Alignment No. 14327
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169
- Alignment No. 14328
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2196: from 56 to 169
- Alignment No. 14329
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2196: from 51 to 169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2197
- Ceres seq\_id 1502544
- Location of start within SEQ ID NO 2195: at 151 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14330
- Ras family
- Location within SEQ ID NO 2197: from 19 to 97 aa.
- Alignment No. 14331
- ADP-ribosylation factor family
- Location within SEQ ID NO 2197: from 2 to 119 aa.
- Alignment No. 14332
- G-protein alpha subunit
- Location within SEQ ID NO 2197: from 44 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14333
- gi No. 1065361
- % Identity 90.8

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- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 2 to 119

- Alignment No. 14334
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14335
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14336
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14337
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2197: from 6 to 119

- Alignment No. 14338
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14339
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14340
- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14341
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14342
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14343
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120

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- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14344  
- gi No. 1703375  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14345  
- gi No. 1703376  
- % Identity 93.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14346  
- gi No. 1703377  
- % Identity 90.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14347  
- gi No. 1703378  
- % Identity 88.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14348  
- gi No. 1703379  
- % Identity 75.7  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2197: from 6 to 119

- Alignment No. 14349  
- gi No. 1703380  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14350  
- gi No. 2129946  
- % Identity 97.7  
- Alignment Length 87  
- Location of Alignment in SEQ ID NO 2197: from 1 to 87

- Alignment No. 14351  
- gi No. 2293566  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14352  
- gi No. 2462736  
- % Identity 97.6  
- Alignment Length 42  
- Location of Alignment in SEQ ID NO 2197: from 1 to 42

- Alignment No. 14353  
- gi No. 2492925  
- % Identity 80  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14354  
- gi No. 2689631  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14355  
- gi No. 283391  
- % Identity 85  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14356  
- gi No. 2852443  
- % Identity 95  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14357  
- gi No. 2854182  
- % Identity 87.4  
- Alignment Length 119  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14358  
- gi No. 3182915  
- % Identity 90.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14359  
- gi No. 3182916  
- % Identity 80.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14360  
- gi No. 3182917  
- % Identity 90.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14361  
- gi No. 3182919  
- % Identity 95.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14362  
- gi No. 3252999  
- % Identity 94.6  
- Alignment Length 93  
- Location of Alignment in SEQ ID NO 2197: from 18 to 110

- Alignment No. 14363  
- gi No. 3746799  
- % Identity 87.3  
- Alignment Length 102  
- Location of Alignment in SEQ ID NO 2197: from 19 to 119



- Alignment No. 14364  
- gi No. 3746801  
- % Identity 86.3  
- Alignment Length 102  
- Location of Alignment in SEQ ID NO 2197: from 19 to 119

- Alignment No. 14365  
- gi No. 4056469  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14366  
- gi No. 4102193  
- % Identity 77.3  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2197: from 1 to 66

- Alignment No. 14367  
- gi No. 4324967  
- % Identity 98.3  
- Alignment Length 117  
- Location of Alignment in SEQ ID NO 2197: from 4 to 119

- Alignment No. 14368  
- gi No. 4502201  
- % Identity 90.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14369  
- gi No. 4502203  
- % Identity 90  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14370  
- gi No. 4502205  
- % Identity 85.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14371  
- gi No. 4502209  
- % Identity 88.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14372  
- gi No. 4502211  
- % Identity 74.8  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2197: from 6 to 119

- Alignment No. 14373  
- gi No. 461532  
- % Identity 89.2  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14374

- gi No. 461533  
- % Identity 89.2  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14375  
- gi No. 4662630  
- % Identity 70.6  
- Alignment Length 119  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14376  
- gi No. 543841  
- % Identity 99.2  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14377  
- gi No. 543842  
- % Identity 90  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14378  
- gi No. 543843  
- % Identity 88.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14379  
- gi No. 543844  
- % Identity 85.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14380  
- gi No. 5579053  
- % Identity 70.7  
- Alignment Length 123  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14381  
- gi No. 728881  
- % Identity 85.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

- Alignment No. 14382  
- gi No. 728883  
- % Identity 74.8  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2197: from 6 to 119

- Alignment No. 14383  
- gi No. 83900  
- % Identity 85  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2197: from 1 to 119

(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2198

- Ceres seq\_id 1502545
- Location of start within SEQ ID NO 2195: at 202 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14384
- Ras family
- Location within SEQ ID NO 2198: from 2 to 80 aa.
- Alignment No. 14385
- ADP-ribosylation factor family
- Location within SEQ ID NO 2198: from 1 to 102 aa.
- Alignment No. 14386
- G-protein alpha subunit
- Location within SEQ ID NO 2198: from 27 to 102 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14387
- gi No. 1065361
- % Identity 90.8
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14388
- gi No. 114121
- % Identity 79
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14389
- gi No. 114122
- % Identity 91.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14390
- gi No. 114124
- % Identity 78.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14391
- gi No. 114128
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14392
- gi No. 114131
- % Identity 74.4
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14393
- gi No. 1168489
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14394

- gi No. 1351973
- % Identity 86.7
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14395
- gi No. 1351974
- % Identity 97.5
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14396
- gi No. 1703373
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14397
- gi No. 1703374
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14398
- gi No. 1703375
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14399
- gi No. 1703376
- % Identity 93.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14400
- gi No. 1703377
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14401
- gi No. 1703378
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14402
- gi No. 1703379
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14403
- gi No. 1703380
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14404
- gi No. 2129946

- % Identity 97.7  
- Alignment Length 87  
- Location of Alignment in SEQ ID NO 2198: from 1 to 70

- Alignment No. 14405  
- gi No. 2293566  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14406  
- gi No. 2462736  
- % Identity 97.6  
- Alignment Length 42  
- Location of Alignment in SEQ ID NO 2198: from 1 to 25

- Alignment No. 14407  
- gi No. 2492925  
- % Identity 80  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14408  
- gi No. 2689631  
- % Identity 98.3  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14409  
- gi No. 283391  
- % Identity 85  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14410  
- gi No. 2852443  
- % Identity 95  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14411  
- gi No. 2854182  
- % Identity 87.4  
- Alignment Length 119  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14412  
- gi No. 3182915  
- % Identity 90.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14413  
- gi No. 3182916  
- % Identity 80.8  
- Alignment Length 120  
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14414  
- gi No. 3182917  
- % Identity 90.8

- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14415
- gi No. 3182919
- % Identity 95.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14416
- gi No. 3252999
- % Identity 94.6
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2198: from 1 to 93
- Alignment No. 14417
- gi No. 3746799
- % Identity 87.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
- Alignment No. 14418
- gi No. 3746801
- % Identity 86.3
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2198: from 2 to 102
- Alignment No. 14419
- gi No. 4056469
- % Identity 98.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14420
- gi No. 4102193
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2198: from 1 to 49
- Alignment No. 14421
- gi No. 4324967
- % Identity 98.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14422
- gi No. 4502201
- % Identity 90.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14423
- gi No. 4502203
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14424
- gi No. 4502205
- % Identity 85.8
- Alignment Length 120

- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14425
- gi No. 4502209
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14426
- gi No. 4502211
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14427
- gi No. 461532
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14428
- gi No. 461533
- % Identity 89.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14429
- gi No. 4662630
- % Identity 70.6
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14430
- gi No. 543841
- % Identity 99.2
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14431
- gi No. 543842
- % Identity 90
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14432
- gi No. 543843
- % Identity 88.3
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14433
- gi No. 543844
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
- Alignment No. 14434
- gi No. 5579053
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

- Alignment No. 14435
- gi No. 728881
- % Identity 85.8
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14436
- gi No. 728883
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2198: from 1 to 102
  
- Alignment No. 14437
- gi No. 83900
- % Identity 85
- Alignment Length 120
- Location of Alignment in SEQ ID NO 2198: from 1 to 102

Maximum Length Sequence corresponding to clone ID 312050

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2199
- Ceres seq\_id 1502573

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2200
- Ceres seq\_id 1502574
- Location of start within SEQ ID NO 2199: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14438
- gi No. 3935181
- % Identity 82.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2200: from 9 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2201
- Ceres seq\_id 1502575
- Location of start within SEQ ID NO 2199: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2202
- Ceres seq\_id 1502576
- Location of start within SEQ ID NO 2199: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14439
- gi No. 3935181
- % Identity 71.7
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2202: from 50 to 161

Maximum Length Sequence corresponding to clone ID 312126



(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2203
- Ceres seq\_id 1502613

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2204
- Ceres seq\_id 1502614
- Location of start within SEQ ID NO 2203: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2205
- Ceres seq\_id 1502615
- Location of start within SEQ ID NO 2203: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14440
- gi No. 3023243
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2205: from 48 to 61

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2206
- Ceres seq\_id 1502616
- Location of start within SEQ ID NO 2203: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14441
- gi No. 3023243
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2206: from 26 to 39

Maximum Length Sequence corresponding to clone ID 312149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2207
- Ceres seq\_id 1502621

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2208
- Ceres seq\_id 1502622
- Location of start within SEQ ID NO 2207: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14442
- gi No. 330442
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 4 to 15
- Alignment No. 14443
- gi No. 3925252
- % Identity 72.7

- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 35 to 45
- Alignment No. 14444
- gi No. 423830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 4 to 15
- Alignment No. 14445
- gi No. 4504731
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
- Alignment No. 14446
- gi No. 4511969
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2208: from 37 to 47
- Alignment No. 14447
- gi No. 4838513
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
- Alignment No. 14448
- gi No. 4838515
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2208: from 38 to 49
- Alignment No. 14449
- gi No. 5305335
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2208: from 34 to 45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2209
- Ceres seq\_id 1502623
- Location of start within SEQ ID NO 2207: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14450
- gi No. 1722778
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2209: from 19 to 30
- Alignment No. 14451
- gi No. 5257260
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2209: from 21 to 35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2210

- Ceres seq\_id 1502624
- Location of start within SEQ ID NO 2207: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14452
- gi No. 102425
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
- Alignment No. 14453
- gi No. 102426
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2210: from 28 to 43
- Alignment No. 14454
- gi No. 1161370
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 26 to 36
- Alignment No. 14455
- gi No. 134950
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2210: from 23 to 35
- Alignment No. 14456
- gi No. 1353462
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 26 to 36
- Alignment No. 14457
- gi No. 1644455
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14458
- gi No. 1644457
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14459
- gi No. 1644459
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14460
- gi No. 1644461
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 28 to 41
- Alignment No. 14461

- gi No. 2108256  
- % Identity 70.6  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2210: from 28 to 43

- Alignment No. 14462  
- gi No. 2143272  
- % Identity 71.4  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2210: from 28 to 40

- Alignment No. 14463  
- gi No. 2257986  
- % Identity 75  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2210: from 26 to 37

- Alignment No. 14464  
- gi No. 2384847  
- % Identity 83.3  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2210: from 22 to 33

- Alignment No. 14465  
- gi No. 2384847  
- % Identity 75  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2210: from 23 to 34

- Alignment No. 14466  
- gi No. 2501953  
- % Identity 76.9  
- Alignment Length 13  
- Location of Alignment in SEQ ID NO 2210: from 28 to 40

- Alignment No. 14467  
- gi No. 2950355  
- % Identity 73.3  
- Alignment Length 15  
- Location of Alignment in SEQ ID NO 2210: from 21 to 35

- Alignment No. 14468  
- gi No. 310574  
- % Identity 90.9  
- Alignment Length 11  
- Location of Alignment in SEQ ID NO 2210: from 27 to 37

- Alignment No. 14469  
- gi No. 310574  
- % Identity 90.9  
- Alignment Length 11  
- Location of Alignment in SEQ ID NO 2210: from 27 to 37

- Alignment No. 14470  
- gi No. 3874146  
- % Identity 72.7  
- Alignment Length 11  
- Location of Alignment in SEQ ID NO 2210: from 27 to 37

- Alignment No. 14471  
- gi No. 4885040

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- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
- Alignment No. 14472
- gi No. 539033
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2210: from 28 to 42
- Alignment No. 14473
- gi No. 5689489
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2210: from 28 to 38
- Alignment No. 14474
- gi No. 871830
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2210: from 28 to 39
- Alignment No. 14475
- gi No. 91094
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2210: from 21 to 34

Maximum Length Sequence corresponding to clone ID 312179

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2211
- Ceres seq\_id 1502635

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2212
- Ceres seq\_id 1502636
- Location of start within SEQ ID NO 2211: at 88 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14476
- Ribosomal protein S28e
- Location within SEQ ID NO 2212: from 1 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14477
- gi No. 1173237
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14478
- gi No. 1313916
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2212: from 6 to 65
- Alignment No. 14479
- gi No. 2739219
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

- Alignment No. 14480
- gi No. 2995699
- % Identity 71.2
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14481
- gi No. 3947719
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14482
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14483
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2212: from 1 to 65
- Alignment No. 14484
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2212: from 3 to 65
- Alignment No. 14485
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2212: from 1 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2213
- Ceres seq\_id 1502637
- Location Of start within SEQ ID NO 2211: at 127 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14486
- Ribosomal protein S28e
- Location within SEQ ID NO 2213: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14487
- gi No. 1173237
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
- Alignment No. 14488
- gi No. 1313916
- % Identity 71.7
- Alignment Length 60
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

- Alignment No. 14489
- gi No. 2739219
- % Identity 92.3
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14490
- gi No. 2995699
- % Identity 71.2
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14491
- gi No. 3947719
- % Identity 87.7
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14492
- gi No. 3947725
- % Identity 86.2
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14493
- gi No. 464714
- % Identity 70.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14494
- gi No. 464715
- % Identity 71.4
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2213: from 1 to 52
  
- Alignment No. 14495
- gi No. 464720
- % Identity 80
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2213: from 1 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2214
- Ceres seq\_id 1502638
- Location of start within SEQ ID NO 2211: at 209 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312184

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2215
- Ceres seq\_id 1502643

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2216
- Ceres seq\_id 1502644
- Location of start within SEQ ID NO 2215: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14496
- Zinc finger, C2H2 type
- Location within SEQ ID NO 2216: from 60 to 82 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14497
- gi No. 1362015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2216: from 57 to 91
- Alignment No. 14498
- gi No. 1362020
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91
- Alignment No. 14499
- gi No. 1362021
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2216: from 57 to 91
- Alignment No. 14500
- gi No. 1871188
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91
- Alignment No. 14501
- gi No. 790687
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2216: from 60 to 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2217
- Ceres seq\_id 1502645
- Location of start within SEQ ID NO 2215: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14502
- Zinc finger, C2H2 type
- Location within SEQ ID NO 2217: from 24 to 46 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14503
- gi No. 1362015
- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2217: from 21 to 55
- Alignment No. 14504
- gi No. 1362020
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55



- Alignment No. 14505
- gi No. 1362021
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2217: from 21 to 55
  
- Alignment No. 14506
- gi No. 1871188
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55
  
- Alignment No. 14507
- gi No. 790687
- % Identity 75
- Alignment Length 32
- Location of Alignment in SEQ ID NO 2217: from 24 to 55

Maximum Length Sequence corresponding to clone ID 312187

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2218
- Ceres seq\_id 1502649

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2219
- Ceres seq\_id 1502650
- Location of start within SEQ ID NO 2218: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14508
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14509
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14510
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14511
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14512
- gi No. 1945621
- % Identity 100
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2219: from 68 to 79
  
- Alignment No. 14513

- gi No. 2947081  
- % Identity 90.9  
- Alignment Length 11  
- Location of Alignment in SEQ ID NO 2219: from 69 to 79

- Alignment No. 14514  
- gi No. 2947081  
- % Identity 85.7  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2219: from 68 to 81

- Alignment No. 14515  
- gi No. 4097820  
- % Identity 83.3  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

- Alignment No. 14516  
- gi No. 4097820  
- % Identity 78.6  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2219: from 68 to 81

- Alignment No. 14517  
- gi No. 4097820  
- % Identity 71.4  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2219: from 67 to 80

- Alignment No. 14518  
- gi No. 539415  
- % Identity 100  
- Alignment Length 11  
- Location of Alignment in SEQ ID NO 2219: from 68 to 78

- Alignment No. 14519  
- gi No. 539415  
- % Identity 91.7  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

- Alignment No. 14520  
- gi No. 539415  
- % Identity 91.7  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

- Alignment No. 14521  
- gi No. 539415  
- % Identity 83.3  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2219: from 68 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2220  
- Ceres seq\_id 1502651  
- Location of start within SEQ ID NO 2218: at 126 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2221
- Ceres seq\_id 1502652
- Location of start within SEQ ID NO 2218: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312195

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2222
- Ceres seq\_id 1502653

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2223
- Ceres seq\_id 1502654
- Location of start within SEQ ID NO 2222: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14522
- gi No. 2894228
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2223: from 9 to 23
- Alignment No. 14523
- gi No. 3378540
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2223: from 4 to 24
- Alignment No. 14524
- gi No. 3660471
- % Identity 87.5
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2223: from 1 to 24
- Alignment No. 14525
- gi No. 4309723
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2223: from 1 to 24

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2224
- Ceres seq\_id 1502655
- Location of start within SEQ ID NO 2222: at 250 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14526
- gi No. 3660471
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2224: from 29 to 46
- Alignment No. 14527

- gi No. 4309723
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2224: from 29 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2225
- Ceres seq\_id 1502656
- Location of start within SEQ ID NO 2222: at 256 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14528
- gi No. 3660471
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2225: from 27 to 44
- Alignment No. 14529
- gi No. 4309723
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2225: from 27 to 44

Maximum Length Sequence corresponding to clone ID 312268

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2226
- Ceres seq\_id 1502682

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2227
- Ceres seq\_id 1502683
- Location of start within SEQ ID NO 2226: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2228
- Ceres seq\_id 1502684
- Location of start within SEQ ID NO 2226: at 117 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14530
- gi No. 462569
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2228: from 65 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2229
- Ceres seq\_id 1502685
- Location of start within SEQ ID NO 2226: at 159 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14531

- gi No. 462569
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2229: from 51 to 61

Maximum Length Sequence corresponding to clone ID 312393

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2230
- Ceres seq\_id 1502713

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2231
- Ceres seq\_id 1502714
- Location of start within SEQ ID NO 2230: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14532
- Asparagine synthase
- Location within SEQ ID NO 2231: from 1 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14533
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2231: from 1 to 145
- Alignment No. 14534
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14535
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2231: from 1 to 134
- Alignment No. 14536
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2231: from 1 to 121
- Alignment No. 14537
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14538
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2231: from 1 to 123
- Alignment No. 14539
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122

- Location of Alignment in SEQ ID NO 2231: from 1 to 122

- Alignment No. 14540

- gi No. 1351988

- % Identity 73.5

- Alignment Length 132

- Location of Alignment in SEQ ID NO 2231: from 1 to 132

- Alignment No. 14541

- gi No. 1617002

- % Identity 81.1

- Alignment Length 122

- Location of Alignment in SEQ ID NO 2231: from 1 to 122

- Alignment No. 14542

- gi No. 1771880

- % Identity 70.3

- Alignment Length 145

- Location of Alignment in SEQ ID NO 2231: from 1 to 145

- Alignment No. 14543

- gi No. 1778370

- % Identity 78

- Alignment Length 123

- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14544

- gi No. 1778372

- % Identity 78.5

- Alignment Length 121

- Location of Alignment in SEQ ID NO 2231: from 1 to 121

- Alignment No. 14545

- gi No. 2429280

- % Identity 83.7

- Alignment Length 123

- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14546

- gi No. 2522320

- % Identity 71.6

- Alignment Length 134

- Location of Alignment in SEQ ID NO 2231: from 1 to 134

- Alignment No. 14547

- gi No. 3132675

- % Identity 79.7

- Alignment Length 123

- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14548

- gi No. 3182921

- % Identity 86.3

- Alignment Length 146

- Location of Alignment in SEQ ID NO 2231: from 1 to 146

- Alignment No. 14549

- gi No. 3821280

- % Identity 80.5

- Alignment Length 123

- Location of Alignment in SEQ ID NO 2231: from 1 to 123

- Alignment No. 14550
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2231: from 1 to 144
- Alignment No. 14551
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2231: from 1 to 139
- Alignment No. 14552
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2231: from 1 to 75
- Alignment No. 14553
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122
- Alignment No. 14554
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2231: from 1 to 122

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2232
- Ceres seq\_id 1502715
- Location of start within SEQ ID NO 2230: at 132 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14555
- Asparagine synthase
- Location within SEQ ID NO 2232: from 1 to 61 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14556
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2232: from 1 to 102
- Alignment No. 14557
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14558
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2232: from 1 to 91

- Alignment No. 14559  
- gi No. 1305549  
- % Identity 80.2  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 2232: from 1 to 78

- Alignment No. 14560  
- gi No. 1351983  
- % Identity 79.7  
- Alignment Length 123  
- Location of Alignment in SEQ ID NO 2232: from 1 to 80

- Alignment No. 14561  
- gi No. 1351985  
- % Identity 78  
- Alignment Length 123  
- Location of Alignment in SEQ ID NO 2232: from 1 to 80

- Alignment No. 14562  
- gi No. 1351987  
- % Identity 80.3  
- Alignment Length 122  
- Location of Alignment in SEQ ID NO 2232: from 1 to 79

- Alignment No. 14563  
- gi No. 1351988  
- % Identity 73.5  
- Alignment Length 132  
- Location of Alignment in SEQ ID NO 2232: from 1 to 89

- Alignment No. 14564  
- gi No. 1617002  
- % Identity 81.1  
- Alignment Length 122  
- Location of Alignment in SEQ ID NO 2232: from 1 to 79

- Alignment No. 14565  
- gi No. 1771880  
- % Identity 70.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2232: from 1 to 102

- Alignment No. 14566  
- gi No. 1778370  
- % Identity 78  
- Alignment Length 123  
- Location of Alignment in SEQ ID NO 2232: from 1 to 80

- Alignment No. 14567  
- gi No. 1778372  
- % Identity 78.5  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 2232: from 1 to 78

- Alignment No. 14568  
- gi No. 2429280  
- % Identity 83.7  
- Alignment Length 123  
- Location of Alignment in SEQ ID NO 2232: from 1 to 80

- Alignment No. 14569



- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2232: from 1 to 91
- Alignment No. 14570
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14571
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 103
- Alignment No. 14572
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2232: from 1 to 80
- Alignment No. 14573
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2232: from 1 to 101
- Alignment No. 14574
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2232: from 1 to 96
- Alignment No. 14575
- gi No. 3913098
- % Identity 80
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2232: from 1 to 32
- Alignment No. 14576
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79
- Alignment No. 14577
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2232: from 1 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2233
- Ceres seq\_id 1502716
- Location of start within SEQ ID NO 2230: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14578

- Asparagine synthase
- Location within SEQ ID NO 2233: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14579
- gi No. 114260
- % Identity 70.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2233: from 1 to 101
- Alignment No. 14580
- gi No. 114261
- % Identity 81.3
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14581
- gi No. 1184265
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2233: from 1 to 90
- Alignment No. 14582
- gi No. 1305549
- % Identity 80.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2233: from 1 to 77
- Alignment No. 14583
- gi No. 1351983
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14584
- gi No. 1351985
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14585
- gi No. 1351987
- % Identity 80.3
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14586
- gi No. 1351988
- % Identity 73.5
- Alignment Length 132
- Location of Alignment in SEQ ID NO 2233: from 1 to 88
- Alignment No. 14587
- gi No. 1617002
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14588
- gi No. 1771880
- % Identity 70.3

- Alignment Length 145
- Location of Alignment in SEQ ID NO 2233: from 1 to 101
- Alignment No. 14589
- gi No. 1778370
- % Identity 78
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14590
- gi No. 1778372
- % Identity 78.5
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2233: from 1 to 77
- Alignment No. 14591
- gi No. 2429280
- % Identity 83.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14592
- gi No. 2522320
- % Identity 71.6
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2233: from 1 to 90
- Alignment No. 14593
- gi No. 3132675
- % Identity 79.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14594
- gi No. 3182921
- % Identity 86.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2233: from 1 to 102
- Alignment No. 14595
- gi No. 3821280
- % Identity 80.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2233: from 1 to 79
- Alignment No. 14596
- gi No. 3859534
- % Identity 77.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2233: from 1 to 100
- Alignment No. 14597
- gi No. 3859536
- % Identity 76.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2233: from 1 to 95
- Alignment No. 14598
- gi No. 3913098
- % Identity 80
- Alignment Length 75

- Location of Alignment in SEQ ID NO 2233: from 1 to 31
- Alignment No. 14599
- gi No. 399064
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78
- Alignment No. 14600
- gi No. 478402
- % Identity 81.1
- Alignment Length 122
- Location of Alignment in SEQ ID NO 2233: from 1 to 78

Maximum Length Sequence corresponding to clone ID 312402

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2234
- Ceres seq\_id 1502717

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2235
- Ceres seq\_id 1502718
- Location of start within SEQ ID NO 2234: at 136 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14601
- gi No. 1778093
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2235: from 1 to 19
- Alignment No. 14602
- gi No. 1778095
- % Identity 73.5
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2235: from 1 to 19
- Alignment No. 14603
- gi No. 4678208
- % Identity 71
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2235: from 1 to 19

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2236
- Ceres seq\_id 1502719
- Location of start within SEQ ID NO 2234: at 172 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2237
- Ceres seq\_id 1502720
- Location of start within SEQ ID NO 2234: at 194 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312407

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2238
- Ceres seq\_id 1502721

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2239
- Ceres seq\_id 1502722
- Location of start within SEQ ID NO 2238: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14604
- gi No. 1705677
- % Identity 76.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2239: from 1 to 108
- Alignment No. 14605
- gi No. 1705678
- % Identity 75.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2239: from 1 to 108
- Alignment No. 14606
- gi No. 2492504
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2239: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2240
- Ceres seq\_id 1502723
- Location of start within SEQ ID NO 2238: at 70 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14607
- gi No. 1705677
- % Identity 76.1
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2240: from 1 to 85
- Alignment No. 14608
- gi No. 1705678
- % Identity 75.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2240: from 1 to 85
- Alignment No. 14609
- gi No. 2492504
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2240: from 1 to 85

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2241
- Ceres seq\_id 1502724
- Location of start within SEQ ID NO 2238: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312409

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2242
- Ceres seq\_id 1502726

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2243
- Ceres seq\_id 1502727
- Location of start within SEQ ID NO 2242: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2244
- Ceres seq\_id 1502728
- Location of start within SEQ ID NO 2242: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14610
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2244: from 21 to 78 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2245
- Ceres seq\_id 1502729
- Location of start within SEQ ID NO 2242: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312432

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2246
- Ceres seq\_id 1502730

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2247
- Ceres seq\_id 1502731
- Location of start within SEQ ID NO 2246: at 114 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14611
- gi No. 2500047
- % Identity 87.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2247: from 15 to 54
- Alignment No. 14612
- gi No. 3510259
- % Identity 73.2

- Alignment Length 56
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14613
- gi No. 4033417
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2247: from 1 to 54
- Alignment No. 14614
- gi No. 4033424
- % Identity 100
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2247: from 1 to 54

Maximum Length Sequence corresponding to clone ID 312476

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2248
- Ceres seq\_id 1502755

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2249
- Ceres seq\_id 1502756
- Location of start within SEQ ID NO 2248: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2250
- Ceres seq\_id 1502757
- Location of start within SEQ ID NO 2248: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14615
- gi No. 2129800
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14616
- gi No. 2129804
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14617
- gi No. 2129805
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14618
- gi No. 2317758
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87
- Alignment No. 14619

- gi No. 2317758
- % Identity 72
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2250: from 65 to 87
  
- Alignment No. 14620
- gi No. 5391446
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2250: from 68 to 87

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2251
- Ceres seq\_id 1502758
- Location of start within SEQ ID NO 2248: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312486

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2252
- Ceres seq\_id 1502759

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2253
- Ceres seq\_id 1502760
- Location of start within SEQ ID NO 2252: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2254
- Ceres seq\_id 1502761
- Location of start within SEQ ID NO 2252: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14621
- gi No. 2781345
- % Identity 79.3
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2254: from 1 to 58
  
- Alignment No. 14622
- gi No. 3157933
- % Identity 76.1
- Alignment Length 71
- Location of Alignment in SEQ ID NO 2254: from 1 to 71

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2255
- Ceres seq\_id 1502762
- Location of start within SEQ ID NO 2252: at 320 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences



Maximum Length Sequence corresponding to clone ID 312499

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2256
- Ceres seq\_id 1502763

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2257
- Ceres seq\_id 1502764
- Location of start within SEQ ID NO 2256: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14623
- gi No. 4512216
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2257: from 114 to 154
- Alignment No. 14624
- gi No. 5689236
- % Identity 75.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2257: from 114 to 154

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2258
- Ceres seq\_id 1502765
- Location of start within SEQ ID NO 2256: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2259
- Ceres seq\_id 1502766
- Location of start within SEQ ID NO 2256: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312502

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2260
- Ceres seq\_id 1502767

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2261
- Ceres seq\_id 1502768
- Location of start within SEQ ID NO 2260: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2262
- Ceres seq\_id 1502769
- Location of start within SEQ ID NO 2260: at 135 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2263
- Ceres seq\_id 1502770
- Location of start within SEQ ID NO 2260: at 250 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14625
- gi No. 5262791
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2263: from 57 to 69

Maximum Length Sequence corresponding to clone ID 312503

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2264
- Ceres seq\_id 1502771

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2265
- Ceres seq\_id 1502772
- Location of start within SEQ ID NO 2264: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14626
- gi No. 2149640
- % Identity 81.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99
- Alignment No. 14627
- gi No. 2959781
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99
- Alignment No. 14628
- gi No. 5107374
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2265: from 1 to 99

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2266
- Ceres seq\_id 1502773
- Location of start within SEQ ID NO 2264: at 146 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14629
- gi No. 2149640
- % Identity 81.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

- Alignment No. 14630
- gi No. 2959781
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51
  
- Alignment No. 14631
- gi No. 5107374
- % Identity 70.7
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2266: from 1 to 51

Maximum Length Sequence corresponding to clone ID 312523

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2267
- Ceres seq\_id 1502781

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2268
- Ceres seq\_id 1502782
- Location of start within SEQ ID NO 2267: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2269
- Ceres seq\_id 1502783
- Location of start within SEQ ID NO 2267: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14632
- gi No. 3264598
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2269: from 19 to 39

Maximum Length Sequence corresponding to clone ID 312525

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2270
- Ceres seq\_id 1502784

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2271
- Ceres seq\_id 1502785
- Location of start within SEQ ID NO 2270: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2272
- Ceres seq\_id 1502786
- Location of start within SEQ ID NO 2270: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2273
- Ceres seq\_id 1502787
- Location of start within SEQ ID NO 2270: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14633
- gi No. 102706
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
  
- Alignment No. 14634
- gi No. 1042189
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19
  
- Alignment No. 14635
- gi No. 1168711
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2273: from 5 to 18
  
- Alignment No. 14636
- gi No. 131044
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
  
- Alignment No. 14637
- gi No. 1362586
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2273: from 4 to 19
  
- Alignment No. 14638
- gi No. 1362587
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19
  
- Alignment No. 14639
- gi No. 1362587
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2273: from 5 to 19

Maximum Length Sequence corresponding to clone ID 312595

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2274
- Ceres seq\_id 1502805

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2275
- Ceres seq\_id 1502806
- Location of start within SEQ ID NO 2274: at 123 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14640
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2275: from 2 to 104 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2276
- Ceres seq\_id 1502807
- Location of start within SEQ ID NO 2274: at 240 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14641
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2276: from 1 to 65 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2277
- Ceres seq\_id 1502808
- Location of start within SEQ ID NO 2274: at 267 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14642
- Macrophage migration inhibitory factor (MIF)
- Location within SEQ ID NO 2277: from 1 to 56 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312598

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2278
- Ceres seq\_id 1502809

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2279
- Ceres seq\_id 1502810
- Location of start within SEQ ID NO 2278: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2280
- Ceres seq\_id 1502811
- Location of start within SEQ ID NO 2278: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14643
- gi No. 4115377
- % Identity 82.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2280: from 58 to 115

Maximum Length Sequence corresponding to clone ID 312622

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2281
- Ceres seq\_id 1502820

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2282
- Ceres seq\_id 1502821
- Location of start within SEQ ID NO 2281: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2283
- Ceres seq\_id 1502822
- Location of start within SEQ ID NO 2281: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14644
- Ribosomal protein S11
- Location within SEQ ID NO 2283: from 28 to 105 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14645
- gi No. 1173200
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2283: from 67 to 105
- Alignment No. 14646
- gi No. 1173201
- % Identity 82.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2283: from 5 to 105
- Alignment No. 14647
- gi No. 131772
- % Identity 92.4
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14648
- gi No. 131773
- % Identity 89.3
- Alignment Length 103
- Location of Alignment in SEQ ID NO 2283: from 3 to 105
- Alignment No. 14649
- gi No. 133771
- % Identity 74.5
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14650
- gi No. 133777
- % Identity 77.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105

- Alignment No. 14651
- gi No. 133782
- % Identity 72.9
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14652
- gi No. 133785
- % Identity 78.3
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14653
- gi No. 1346941
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14654
- gi No. 1350935
- % Identity 74.8
- Alignment Length 107
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14655
- gi No. 2350992
- % Identity 77
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2283: from 27 to 100
- Alignment No. 14656
- gi No. 2414647
- % Identity 80.5
- Alignment Length 87
- Location of Alignment in SEQ ID NO 2283: from 16 to 102
- Alignment No. 14657
- gi No. 2500442
- % Identity 70.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2283: from 4 to 80
- Alignment No. 14658
- gi No. 2500443
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2283: from 85 to 105
- Alignment No. 14659
- gi No. 3097244
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14660
- gi No. 3122785
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14661

- gi No. 4574240
- % Identity 77.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14662
- gi No. 4588920
- % Identity 74.5
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14663
- gi No. 4678226
- % Identity 84.8
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14664
- gi No. 4886269
- % Identity 85.7
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14665
- gi No. 5032051
- % Identity 79.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14666
- gi No. 5441523
- % Identity 88.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2283: from 72 to 105
- Alignment No. 14667
- gi No. 547604
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14668
- gi No. 70946
- % Identity 74.1
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14669
- gi No. 730453
- % Identity 75.3
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2283: from 21 to 105
- Alignment No. 14670
- gi No. 730633
- % Identity 76.4
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2283: from 1 to 105
- Alignment No. 14671
- gi No. 83794



- % Identity 74.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2283: from 1 to 105

Maximum Length Sequence corresponding to clone ID 312649

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2284
- Ceres seq\_id 1502834

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2285
- Ceres seq\_id 1502835
- Location of start within SEQ ID NO 2284: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14672
- Forkhead-associated (FHA) domain
- Location within SEQ ID NO 2285: from 92 to 145 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2286
- Ceres seq\_id 1502836
- Location of start within SEQ ID NO 2284: at 57 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14673
- Forkhead-associated (FHA) domain
- Location within SEQ ID NO 2286: from 74 to 127 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312672

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2287
- Ceres seq\_id 1502844

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2288
- Ceres seq\_id 1502845
- Location of start within SEQ ID NO 2287: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14674
- DnaJ domain
- Location within SEQ ID NO 2288: from 1 to 29 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2289
- Ceres seq\_id 1502850

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2290
- Ceres seq\_id 1502851
- Location of start within SEQ ID NO 2289: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2291
- Ceres seq\_id 1502852
- Location of start within SEQ ID NO 2289: at 144 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2292
- Ceres seq\_id 1502853
- Location of start within SEQ ID NO 2289: at 217 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14675
- gi No. 4220472
- % Identity 76.3
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2292: from 1 to 19

Maximum Length Sequence corresponding to clone ID 312744

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2293
- Ceres seq\_id 1502860

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2294
- Ceres seq\_id 1502861
- Location of start within SEQ ID NO 2293: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2295
- Ceres seq\_id 1502862
- Location of start within SEQ ID NO 2293: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 14676
- Plant lipid transfer protein family
- Location within SEQ ID NO 2295: from 75 to 153 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14677
- gi No. 1084462
- % Identity 70
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2295: from 75 to 152
- Alignment No. 14678
- gi No. 2226329
- % Identity 93.8

- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154
- Alignment No. 14679
- gi No. 399204
- % Identity 92.5
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2295: from 75 to 154

Maximum Length Sequence corresponding to clone ID 312842

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2296
- Ceres seq\_id 1502896

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2297
- Ceres seq\_id 1502897
- Location of start within SEQ ID NO 2296: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14680
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2297: from 1 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14681
- gi No. 100610
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14682
- gi No. 100611
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14683
- gi No. 1076633
- % Identity 88.3
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14684
- gi No. 1082205
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
- Alignment No. 14685
- gi No. 1216280
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
- Alignment No. 14686
- gi No. 1216285
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14687
- gi No. 134588
- % Identity 72.5
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2297: from 1 to 109
  
- Alignment No. 14688
- gi No. 1362153
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
  
- Alignment No. 14689
- gi No. 1362154
- % Identity 100
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
  
- Alignment No. 14690
- gi No. 1362155
- % Identity 96.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2297: from 1 to 28
  
- Alignment No. 14691
- gi No. 1477684
- % Identity 94.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14692
- gi No. 1703034
- % Identity 72.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2297: from 2 to 109
  
- Alignment No. 14693
- gi No. 1729444
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14694
- gi No. 1742967
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14695
- gi No. 1743009
- % Identity 91
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14696
- gi No. 1935916
- % Identity 89.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2297: from 1 to 110
  
- Alignment No. 14697

- gi No. 2130048  
- % Identity 96.4  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14698  
- gi No. 2136044  
- % Identity 75  
- Alignment Length 32  
- Location of Alignment in SEQ ID NO 2297: from 3 to 34

- Alignment No. 14699  
- gi No. 2137442  
- % Identity 94.1  
- Alignment Length 34  
- Location of Alignment in SEQ ID NO 2297: from 1 to 34

- Alignment No. 14700  
- gi No. 2146759  
- % Identity 100  
- Alignment Length 28  
- Location of Alignment in SEQ ID NO 2297: from 1 to 28

- Alignment No. 14701  
- gi No. 2146812  
- % Identity 78.4  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14702  
- gi No. 2274869  
- % Identity 97.2  
- Alignment Length 36  
- Location of Alignment in SEQ ID NO 2297: from 5 to 40

- Alignment No. 14703  
- gi No. 2499626  
- % Identity 72.5  
- Alignment Length 109  
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14704  
- gi No. 2507201  
- % Identity 71.8  
- Alignment Length 110  
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14705  
- gi No. 3023235  
- % Identity 86.7  
- Alignment Length 30  
- Location of Alignment in SEQ ID NO 2297: from 2 to 31

- Alignment No. 14706  
- gi No. 322596  
- % Identity 92.8  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14707  
- gi No. 3341452

- % Identity 79.3  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14708  
- gi No. 400982  
- % Identity 82.9  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14709  
- gi No. 4091885  
- % Identity 93.7  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14710  
- gi No. 4099088  
- % Identity 78.4  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14711  
- gi No. 4107001  
- % Identity 96.4  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14712  
- gi No. 4107003  
- % Identity 96.4  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14713  
- gi No. 4107005  
- % Identity 96.4  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14714  
- gi No. 4107009  
- % Identity 95.5  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14715  
- gi No. 4432983  
- % Identity 70  
- Alignment Length 40  
- Location of Alignment in SEQ ID NO 2297: from 8 to 47

- Alignment No. 14716  
- gi No. 4520332  
- % Identity 74.3  
- Alignment Length 109  
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14717  
- gi No. 4567091  
- % Identity 92.8

- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14718  
- gi No. 4982468  
- % Identity 75.2  
- Alignment Length 109  
- Location of Alignment in SEQ ID NO 2297: from 2 to 110

- Alignment No. 14719  
- gi No. 5410312  
- % Identity 72.2  
- Alignment Length 108  
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14720  
- gi No. 5442424  
- % Identity 72.5  
- Alignment Length 109  
- Location of Alignment in SEQ ID NO 2297: from 1 to 109

- Alignment No. 14721  
- gi No. 5453964  
- % Identity 71.3  
- Alignment Length 108  
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14722  
- gi No. 5453966  
- % Identity 71.3  
- Alignment Length 108  
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14723  
- gi No. 575292  
- % Identity 96.4  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2297: from 1 to 110

- Alignment No. 14724  
- gi No. 728758  
- % Identity 72.2  
- Alignment Length 108  
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

- Alignment No. 14725  
- gi No. 862473  
- % Identity 72.2  
- Alignment Length 108  
- Location of Alignment in SEQ ID NO 2297: from 2 to 109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2298  
- Ceres seq\_id 1502898  
- Location of start within SEQ ID NO 2296: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 312860

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2299
- Ceres seq\_id 1502902

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2300
- Ceres seq\_id 1502903
- Location of start within SEQ ID NO 2299: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14726
- gi No. 2160438
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
  
- Alignment No. 14727
- gi No. 286238
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
  
- Alignment No. 14728
- gi No. 348497
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76
  
- Alignment No. 14729
- gi No. 548375
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2300: from 66 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2301
- Ceres seq\_id 1502904
- Location of start within SEQ ID NO 2299: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14730
- gi No. 3413810
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2301: from 26 to 37

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2302
- Ceres seq\_id 1502905
- Location of start within SEQ ID NO 2299: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14731
- gi No. 2160438
- % Identity 72.7
- Alignment Length 11



- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14732
- gi No. 286238
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14733
- gi No. 348497
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61
- Alignment No. 14734
- gi No. 548375
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2302: from 51 to 61

Maximum Length Sequence corresponding to clone ID 312920

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2303
- Ceres seq\_id 1502937

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2304
- Ceres seq\_id 1502938
- Location Of start within SEQ ID NO 2303: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14735
- gi No. 3367741
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2304: from 85 to 96

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2305
- Ceres seq\_id 1502939
- Location of start within SEQ ID NO 2303: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14736
- Nuclear transition protein 2
- Location within SEQ ID NO 2305: from 7 to 72 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2306
- Ceres seq\_id 1502940
- Location of start within SEQ ID NO 2303: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2307
- Ceres seq\_id 1502981

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2308
- Ceres seq\_id 1502982
- Location of start within SEQ ID NO 2307: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14737
- gi No. 465445
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2308: from 107 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2309
- Ceres seq\_id 1502983
- Location of start within SEQ ID NO 2307: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2310
- Ceres seq\_id 1502984
- Location of start within SEQ ID NO 2307: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14738
- gi No. 102706
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118
- Alignment No. 14739
- gi No. 102706
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14740
- gi No. 102706
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14741
- gi No. 102706
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14742
- gi No. 102707
- % Identity 92.3

- Alignment Length 13  
- Location of Alignment in SEQ ID NO 2310: from 107 to 119

- Alignment No. 14743  
- gi No. 1170389  
- % Identity 85.7  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14744  
- gi No. 1170392  
- % Identity 85.7  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14745  
- gi No. 1170396  
- % Identity 70.6  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14746  
- gi No. 1170397  
- % Identity 70.6  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14747  
- gi No. 1170398  
- % Identity 70.6  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14748  
- gi No. 1170401  
- % Identity 78.6  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 108 to 119

- Alignment No. 14749  
- gi No. 1170405  
- % Identity 85.7  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14750  
- gi No. 1170406  
- % Identity 85.7  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14751  
- gi No. 123689  
- % Identity 92.9  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14752  
- gi No. 123689  
- % Identity 82.4  
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2310: from 106 to 122

- Alignment No. 14753  
- gi No. 123695  
- % Identity 92.3  
- Alignment Length 13  
- Location of Alignment in SEQ ID NO 2310: from 107 to 119

- Alignment No. 14754  
- gi No. 131040  
- % Identity 81.8  
- Alignment Length 11  
- Location of Alignment in SEQ ID NO 2310: from 107 to 117

- Alignment No. 14755  
- gi No. 131040  
- % Identity 81.8  
- Alignment Length 11  
- Location of Alignment in SEQ ID NO 2310: from 108 to 118

- Alignment No. 14756  
- gi No. 131044  
- % Identity 92.3  
- Alignment Length 13  
- Location of Alignment in SEQ ID NO 2310: from 106 to 118

- Alignment No. 14757  
- gi No. 131044  
- % Identity 78.6  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14758  
- gi No. 131044  
- % Identity 86.7  
- Alignment Length 15  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14759  
- gi No. 131044  
- % Identity 76.5  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14760  
- gi No. 163635  
- % Identity 92.9  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14761  
- gi No. 163635  
- % Identity 85.7  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2310: from 106 to 119

- Alignment No. 14762  
- gi No. 163635  
- % Identity 82.4  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2310: from 106 to 122

- Alignment No. 14763
- gi No. 2134213
- % Identity 92.3
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 107 to 119
- Alignment No. 14764
- gi No. 2134213
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14765
- gi No. 225057
- % Identity 92.9
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2310: from 106 to 119
- Alignment No. 14766
- gi No. 225057
- % Identity 82.4
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2310: from 106 to 122
- Alignment No. 14767
- gi No. 357984
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118
- Alignment No. 14768
- gi No. 5456964
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2310: from 106 to 118
- Alignment No. 14769
- gi No. 85630
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 107 to 117
- Alignment No. 14770
- gi No. 85630
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2310: from 108 to 118

Maximum Length Sequence corresponding to clone ID 313054

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2311
- Ceres seq\_id 1502985

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2312
- Ceres seq\_id 1502986
- Location of start within SEQ ID NO 2311: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14771

- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2312: from 21 to 102 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2313
- Ceres seq\_id 1502987
- Location of start within SEQ ID NO 2311: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313104

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2314
- Ceres seq\_id 1503000

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2315
- Ceres seq\_id 1503001
- Location of start within SEQ ID NO 2314: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2316
- Ceres seq\_id 1503002
- Location of start within SEQ ID NO 2314: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14772
- CRAL/TRIO domain.
- Location within SEQ ID NO 2316: from 7 to 80 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313149

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2317
- Ceres seq\_id 1503010

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2318
- Ceres seq\_id 1503011
- Location of start within SEQ ID NO 2317: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14773
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2318: from 58 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2319
- Ceres seq\_id 1503012
- Location of start within SEQ ID NO 2317: at 77 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14774
- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 2319: from 33 to 81 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313273

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2320
- Ceres seq\_id 1503042

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2321
- Ceres seq\_id 1503043
- Location of start within SEQ ID NO 2320: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14775
- gi No. 2529670
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2321: from 24 to 39
- Alignment No. 14776
- gi No. 3021348
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2321: from 26 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2322
- Ceres seq\_id 1503044
- Location of start within SEQ ID NO 2320: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14777
- gi No. 2529670
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2322: from 2 to 17
- Alignment No. 14778
- gi No. 3021348
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2322: from 4 to 18

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2323
- Ceres seq\_id 1503045
- Location of start within SEQ ID NO 2320: at 225 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14779

- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2323: from 1 to 51 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14780
- gi No. 1172977
- % Identity 72.3
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2323: from 1 to 49
- Alignment No. 14781
- gi No. 2529670
- % Identity 73.1
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2323: from 1 to 44

Maximum Length Sequence corresponding to clone ID 313280

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2324
- Ceres seq\_id 1503048

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2325
- Ceres seq\_id 1503049
- Location of start within SEQ ID NO 2324: at 85 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14782
- gi No. 1171036
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14783
- gi No. 1480016
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14784
- gi No. 2407331
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14785
- gi No. 2497887
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14786
- gi No. 2497888
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14787
- gi No. 2497890
- % Identity 77.8



- Alignment Length 18
- Location of Alignment in SEQ ID NO 2325: from 1 to 18
- Alignment No. 14788
- gi No. 2497892
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14789
- gi No. 2497893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14790
- gi No. 2497895
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14791
- gi No. 2497901
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14792
- gi No. 2497903
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14793
- gi No. 2497904
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14794
- gi No. 2507587
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14795
- gi No. 266579
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14796
- gi No. 3694984
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14797
- gi No. 3900980
- % Identity 70
- Alignment Length 20

- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14798
- gi No. 3901014
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14799
- gi No. 4877893
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20
- Alignment No. 14800
- gi No. 72178
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2325: from 1 to 20

Maximum Length Sequence corresponding to clone ID 313319

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2326
- Ceres seq\_id 1503064

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2327
- Ceres seq\_id 1503065
- Location of start within SEQ ID NO 2326: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 14801
- Fatty acid desaturase
- Location within SEQ ID NO 2327: from 37 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14802
- gi No. 4104056
- % Identity 71.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 2327: from 5 to 169

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2328
- Ceres seq\_id 1503066
- Location of start within SEQ ID NO 2326: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14803
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
- Alignment No. 14804
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

- Alignment No. 14805
- gi No. 100214
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
- Alignment No. 14806
- gi No. 1185397
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15
- Alignment No. 14807
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14808
- gi No. 1185397
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14809
- gi No. 168237
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15
- Alignment No. 14810
- gi No. 2429362
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2328: from 5 to 15
- Alignment No. 14811
- gi No. 4096360
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2328: from 4 to 15
- Alignment No. 14812
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14813
- gi No. 4096360
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2328: from 3 to 15
- Alignment No. 14814
- gi No. 5430752
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2328: from 2 to 15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2329
- Ceres seq\_id 1503067
- Location of start within SEQ ID NO 2326: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14815
- Fatty acid desaturase
- Location within SEQ ID NO 2329: from 1 to 90 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14816
- gi No. 4104056
- % Identity 71.7
- Alignment Length 166
- Location of Alignment in SEQ ID NO 2329: from 1 to 131

Maximum Length Sequence corresponding to clone ID 313321

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2330
- Ceres seq\_id 1503071

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2331
- Ceres seq\_id 1503072
- Location of start within SEQ ID NO 2330: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14817
- gi No. 3850569
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2331: from 16 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2332
- Ceres seq\_id 1503073
- Location of start within SEQ ID NO 2330: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313406

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2333
- Ceres seq\_id 1503104

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2334
- Ceres seq\_id 1503105
- Location of start within SEQ ID NO 2333: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14818
- gi No. 2564066
- % Identity 78.5
- Alignment Length 65

- Location of Alignment in SEQ ID NO 2334: from 38 to 102
- Alignment No. 14819
- gi No. 5031275
- % Identity 70.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2334: from 38 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2335
- Ceres seq\_id 1503106
- Location of start within SEQ ID NO 2333: at 112 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14820
- gi No. 2564066
- % Identity 78.5
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2335: from 1 to 65
- Alignment No. 14821
- gi No. 5031275
- % Identity 70.8
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2335: from 1 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2336
- Ceres seq\_id 1503107
- Location of start within SEQ ID NO 2333: at 222 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14822
- gi No. 2464905
- % Identity 77.8
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2336: from 29 to 63
- Alignment No. 14823
- gi No. 2564066
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63
- Alignment No. 14824
- gi No. 3269288
- % Identity 86.5
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63
- Alignment No. 14825
- gi No. 5031275
- % Identity 83.8
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2336: from 28 to 63

Maximum Length Sequence corresponding to clone ID 313421

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2337
- Ceres seq\_id 1503108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2338
- Ceres seq\_id 1503109
- Location of start within SEQ ID NO 2337: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14826
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2338: from 38 to 145 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14827
- gi No. 1161254
- % Identity 83.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14828
- gi No. 1168529
- % Identity 80.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14829
- gi No. 1168530
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14830
- gi No. 1362002
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14831
- gi No. 1362026
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14832
- gi No. 1362050
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14833
- gi No. 1362051
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14834
- gi No. 1669573
- % Identity 93.8
- Alignment Length 112

- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14835
- gi No. 1944000
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14836
- gi No. 2055374
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14837
- gi No. 2129803
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14838
- gi No. 2146746
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14839
- gi No. 3046731
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14840
- gi No. 310580
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14841
- gi No. 3169176
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2338: from 36 to 148
- Alignment No. 14842
- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2338: from 31 to 145
- Alignment No. 14843
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145
- Alignment No. 14844
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2338: from 34 to 145

- Alignment No. 14845
- gi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2338: from 45 to 145
- Alignment No. 14846
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145
- Alignment No. 14847
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2338: from 36 to 145

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2339
- Ceres seq\_id 1503110
- Location of start within SEQ ID NO 2337: at 102 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14848
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2339: from 5 to 112 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14849
- gi No. 1161254
- % Identity 83.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14850
- gi No. 1168529
- % Identity 80.9
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14851
- gi No. 1168530
- % Identity 77.3
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14852
- gi No. 1362002
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14853
- gi No. 1362026
- % Identity 80
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112



- Alignment No. 14854
- gi No. 1362050
- % Identity 83
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14855
- gi No. 1362051
- % Identity 84.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14856
- gi No. 1669573
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14857
- gi No. 1944000
- % Identity 93.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14858
- gi No. 2055374
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14859
- gi No. 2129803
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14860
- gi No. 2146746
- % Identity 77.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14861
- gi No. 3046731
- % Identity 81.8
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14862
- gi No. 310580
- % Identity 82.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14863
- gi No. 3169176
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2339: from 3 to 115
- Alignment No. 14864

- gi No. 3297819
- % Identity 78.4
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14865
- gi No. 3811293
- % Identity 84.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14866
- gi No. 4098174
- % Identity 85.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2339: from 1 to 112
- Alignment No. 14867
- gi No. 416564
- % Identity 80.2
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2339: from 12 to 112
- Alignment No. 14868
- gi No. 4490752
- % Identity 76.4
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112
- Alignment No. 14869
- gi No. 481002
- % Identity 74.5
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2339: from 3 to 112

Maximum Length Sequence corresponding to clone ID 313476

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2340
- Ceres seq\_id 1503132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2341
- Ceres seq\_id 1503133
- Location of start within SEQ ID NO 2340: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2342
- Ceres seq\_id 1503134
- Location of start within SEQ ID NO 2340: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14870
- gi No. 547305
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2342: from 32 to 51

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2343
- Ceres seq\_id 1503135
- Location of start within SEQ ID NO 2340: at 122 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14871
- gi No. 547305
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2343: from 18 to 37

Maximum Length Sequence corresponding to clone ID 313477

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2344
- Ceres seq\_id 1503136

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2345
- Ceres seq\_id 1503137
- Location of start within SEQ ID NO 2344: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14872
- gi No. 103026
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2345: from 4 to 14

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2346
- Ceres seq\_id 1503138
- Location of start within SEQ ID NO 2344: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14873
- gi No. 1869859
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2346: from 64 to 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2347
- Ceres seq\_id 1503139
- Location of start within SEQ ID NO 2344: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14874
- gi No. 1869859
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2347: from 51 to 62

Maximum Length Sequence corresponding to clone ID 313513

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2348
- Ceres seq\_id 1503144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2349
- Ceres seq\_id 1503145
- Location of start within SEQ ID NO 2348: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14875
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2349: from 28 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2350
- Ceres seq\_id 1503146
- Location of start within SEQ ID NO 2348: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14876
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2350: from 22 to 102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2351
- Ceres seq\_id 1503147
- Location of start within SEQ ID NO 2348: at 137 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14877
- gi No. 3426262
- % Identity 72.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2351: from 1 to 63

Maximum Length Sequence corresponding to clone ID 313560

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2352
- Ceres seq\_id 1503148

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2353
- Ceres seq\_id 1503149
- Location of start within SEQ ID NO 2352: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14878
- gi No. 1351999
- % Identity 81

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2353: from 1 to 21
- Alignment No. 14879
- gi No. 2129613
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2353: from 1 to 23
- Alignment No. 14880
- gi No. 3096930
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19
- Alignment No. 14881
- gi No. 4510417
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2353: from 1 to 22
- Alignment No. 14882
- gi No. 4544389
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2353: from 1 to 19
- Alignment No. 14883
- gi No. 5678605
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2353: from 1 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2354
- Ceres seq\_id 1503150
- Location of start within SEQ ID NO 2352: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313561

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2355
- Ceres seq\_id 1503151

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2356
- Ceres seq\_id 1503152
- Location of start within SEQ ID NO 2355: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2357
- Ceres seq\_id 1503153
- Location of start within SEQ ID NO 2355: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2358
- Ceres seq\_id 1503154
- Location of start within SEQ ID NO 2355: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14884
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2358: from 5 to 95 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313590

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2359
- Ceres seq\_id 1503160

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2360
- Ceres seq\_id 1503161
- Location of start within SEQ ID NO 2359: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14885
- gi No. 5689238
- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2360: from 108 to 150

Maximum Length Sequence corresponding to clone ID 313616

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2361
- Ceres seq\_id 1503170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2362
- Ceres seq\_id 1503171
- Location of start within SEQ ID NO 2361: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14886
- Integrase
- Location within SEQ ID NO 2362: from 58 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2363
- Ceres seq\_id 1503172
- Location of start within SEQ ID NO 2361: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14887
- Integrase

- Location within SEQ ID NO 2363: from 58 to 125 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313650

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2364
- Ceres seq\_id 1503191

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2365
- Ceres seq\_id 1503192
- Location of start within SEQ ID NO 2364: at 37 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14888
- gi No. 102707
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2365: from 115 to 126
- Alignment No. 14889
- gi No. 3153821
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2365: from 13 to 26
- Alignment No. 14890
- gi No. 5032119
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2365: from 13 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2366
- Ceres seq\_id 1503193
- Location of start within SEQ ID NO 2364: at 134 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313677

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2367
- Ceres seq\_id 1503200

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2368
- Ceres seq\_id 1503201
- Location of start within SEQ ID NO 2367: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14891
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2368: from 73 to 151 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2369
- Ceres seq\_id 1503202
- Location of start within SEQ ID NO 2367: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14892
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2369: from 73 to 151 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2370
- Ceres seq\_id 1503203
- Location of start within SEQ ID NO 2367: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14893
- DEAD/DEAH box helicase
- Location within SEQ ID NO 2370: from 38 to 116 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313754

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2371
- Ceres seq\_id 1503237

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2372
- Ceres seq\_id 1503238
- Location of start within SEQ ID NO 2371: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14894
- gi No. 1710490
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14895
- gi No. 2245098
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2372: from 24 to 40
- Alignment No. 14896
- gi No. 2982249
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
- Alignment No. 14897
- gi No. 2982318
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40



- Alignment No. 14898
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14899
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14900
- gi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14901
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40
  
- Alignment No. 14902
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2372: from 22 to 40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2373
- Ceres seq\_id 1503239
- Location of start within SEQ ID NO 2371: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2374
- Ceres seq\_id 1503240
- Location of start within SEQ ID NO 2371: at 64 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14903
- gi No. 1710490
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
  
- Alignment No. 14904
- gi No. 2245098
- % Identity 94.1
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2374: from 3 to 19
  
- Alignment No. 14905
- gi No. 2982249

- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14906
- gi No. 2982318
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14907
- gi No. 3122673
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14908
- gi No. 3608479
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14909
- gi No. 4506593
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14910
- gi No. 730532
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19
- Alignment No. 14911
- gi No. 730533
- % Identity 84.2
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2374: from 1 to 19

Maximum Length Sequence corresponding to clone ID 313846

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2375
- Ceres seq\_id 1503268

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2376
- Ceres seq\_id 1503269
- Location of start within SEQ ID NO 2375: at 197 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14912
- gi No. 2062167
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2376: from 24 to 62

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2377
- Ceres seq\_id 1503270

- Location of start within SEQ ID NO 2375: at 266 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14913
- gi No. 2062167
- % Identity 74.4
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2377: from 1 to 39

Maximum Length Sequence corresponding to clone ID 313854

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2378
- Ceres seq\_id 1503275

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2379
- Ceres seq\_id 1503276
- Location of start within SEQ ID NO 2378: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14914
- gi No. 1174492
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14915
- gi No. 2494300
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14916
- gi No. 2832707
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14917
- gi No. 3142294
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2379: from 39 to 83
- Alignment No. 14918
- gi No. 3790165
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83
- Alignment No. 14919
- gi No. 3790184
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83
- Alignment No. 14920
- gi No. 4185138

- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2379: from 42 to 83
- Alignment No. 14921
- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2379: from 44 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2380
- Ceres seq\_id 1503277
- Location of start within SEQ ID NO 2378: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14922
- gi No. 1174492
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14923
- gi No. 2494300
- % Identity 76.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14924
- gi No. 2832707
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14925
- gi No. 3142294
- % Identity 78.3
- Alignment Length 46
- Location of Alignment in SEQ ID NO 2380: from 1 to 45
- Alignment No. 14926
- gi No. 3790165
- % Identity 72.5
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
- Alignment No. 14927
- gi No. 3790184
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
- Alignment No. 14928
- gi No. 4185138
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2380: from 4 to 45
- Alignment No. 14929

```
- gi No. 4503507
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2380: from 6 to 45
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2381
- Ceres seq\_id 1503278
- Location of start within SEQ ID NO 2378: at 233 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14930
- Elongation factor Tu family
- Location within SEQ ID NO 2381: from 4 to 76 aa.

#### (D) Related Amino Acid Sequences

- Alignment No. 14931
- gi No. 1174492
- % Identity 82.1
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2381: from 4 to 42

```
- Alignment No. 14932
- gi No. 2494300
- % Identity 76.6
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2381: from 4 to 67
```

- Alignment No. 14933
- gi No. 2494301
- % Identity 77.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2381: from 4 to 69

- Alignment No. 14934
- gi No. 2832707
- % Identity 89.2
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76

```
- Alignment No. 14935
- gi No. 3142294
- % Identity 90.5
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
```

- Alignment No. 14936
- gi No. 3790165
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2381: from 4 to 76

```
- Alignment No. 14937
- gi No. 3790184
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEO ID NO 2381: from 4 to 71
```

- Alignment No. 14938
- qi No. 417179

Case	Age	Sex	Duration	Location	Findings	Comments
1	10	M	10 days	Left eye	Small, dark, pigmented lesion	Benign
2	15	F	2 weeks	Right eye	Large, white, fibrous lesion	Benign
3	20	M	3 months	Left eye	Small, dark, pigmented lesion	Benign
4	25	F	6 months	Right eye	Large, white, fibrous lesion	Benign
5	30	M	1 year	Left eye	Small, dark, pigmented lesion	Benign
6	35	F	1.5 years	Right eye	Large, white, fibrous lesion	Benign
7	40	M	2 years	Left eye	Small, dark, pigmented lesion	Benign
8	45	F	2.5 years	Right eye	Large, white, fibrous lesion	Benign
9	50	M	3 years	Left eye	Small, dark, pigmented lesion	Benign
10	55	F	3.5 years	Right eye	Large, white, fibrous lesion	Benign
11	60	M	4 years	Left eye	Small, dark, pigmented lesion	Benign
12	65	F	4.5 years	Right eye	Large, white, fibrous lesion	Benign
13	70	M	5 years	Left eye	Small, dark, pigmented lesion	Benign
14	75	F	5.5 years	Right eye	Large, white, fibrous lesion	Benign
15	80	M	6 years	Left eye	Small, dark, pigmented lesion	Benign
16	85	F	6.5 years	Right eye	Large, white, fibrous lesion	Benign
17	90	M	7 years	Left eye	Small, dark, pigmented lesion	Benign
18	95	F	7.5 years	Right eye	Large, white, fibrous lesion	Benign
19	100	M	8 years	Left eye	Small, dark, pigmented lesion	Benign
20	105	F	8.5 years	Right eye	Large, white, fibrous lesion	Benign

- % Identity 73.5
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71
- Alignment No. 14939
- gi No. 4185138
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2381: from 4 to 76
- Alignment No. 14940
- gi No. 4503507
- % Identity 75
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2381: from 4 to 71

Maximum Length Sequence corresponding to clone ID 313864

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2382
- Ceres seq\_id 1503279

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2383
- Ceres seq\_id 1503280
- Location of start within SEQ ID NO 2382: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14941
- gi No. 4512664
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14942
- gi No. 4874278
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14943
- gi No. 4902470
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14944
- gi No. 4902877
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15
- Alignment No. 14945
- gi No. 4902879
- % Identity 93.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2383: from 1 to 15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2384
- Ceres seq\_id 1503281

- Location of start within SEQ ID NO 2382: at 98 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2385
- Ceres seq\_id 1503282
- Location of start within SEQ ID NO 2382: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14946
- gi No. 4512664
- % Identity 70.6
- Alignment Length 85
- Location of Alignment in SEQ ID NO 2385: from 1 to 49

Maximum Length Sequence corresponding to clone ID 313894

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2386
- Ceres seq\_id 1503297

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2387
- Ceres seq\_id 1503298
- Location of start within SEQ ID NO 2386: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14947
- C2 domain
- Location within SEQ ID NO 2387: from 27 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 313912

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2388
- Ceres seq\_id 1503299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2389
- Ceres seq\_id 1503300
- Location of start within SEQ ID NO 2388: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14948
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2389: from 1 to 54 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14949
- gi No. 2191149
- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
- Alignment No. 14950
- gi No. 2505874

- % Identity 74
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
- Alignment No. 14951
- gi No. 3482919
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54
- Alignment No. 14952
- gi No. 4204849
- % Identity 70
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2389: from 1 to 50
- Alignment No. 14953
- gi No. 4263791
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2389: from 1 to 79
- Alignment No. 14954
- gi No. 4512659
- % Identity 70.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2389: from 1 to 54
- Alignment No. 14955
- gi No. 4836880
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56
- Alignment No. 14956
- gi No. 5042449
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2389: from 1 to 56

Maximum Length Sequence corresponding to clone ID 313922

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2390
- Ceres seq\_id 1503305

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2391
- Ceres seq\_id 1503306
- Location of start within SEQ ID NO 2390: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2392
- Ceres seq\_id 1503307
- Location of start within SEQ ID NO 2390: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14957



- Major intrinsic protein
  - Location within SEQ ID NO 2392: from 35 to 135 aa.
- (D) Related Amino Acid Sequences
- Alignment No. 14958
  - gi No. 1076687
  - % Identity 80.2
  - Alignment Length 106
  - Location of Alignment in SEQ ID NO 2392: from 30 to 135
- Alignment No. 14959
- gi No. 1212915
- % Identity 71.7
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14960
- gi No. 1212921
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14961
- gi No. 1212923
- % Identity 72.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14962
- gi No. 126959
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14963
- gi No. 1518057
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14964
- gi No. 1743369
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14965
- gi No. 1794147
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14966
- gi No. 2058706
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14967
- gi No. 2245093
- % Identity 74.3

- Alignment Length 113
- Location of Alignment in SEQ ID NO 2392: from 25 to 137
- Alignment No. 14968
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14969
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14970
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14971
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2392: from 103 to 137
- Alignment No. 14972
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2392: from 25 to 135
- Alignment No. 14973
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2392: from 69 to 137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2393
- Ceres seq\_id 1503308
- Location of start within SEQ ID NO 2390: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14974
- Major intrinsic protein
- Location within SEQ ID NO 2393: from 11 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 14975
- gi No. 1076687
- % Identity 80.2
- Alignment Length 106
- Location of Alignment in SEQ ID NO 2393: from 6 to 111
- Alignment No. 14976
- gi No. 1212915
- % Identity 71.7
- Alignment Length 113

- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14977
- gi No. 1212921
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14978
- gi No. 1212923
- % Identity 72.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14979
- gi No. 126959
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14980
- gi No. 1518057
- % Identity 78.4
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14981
- gi No. 1743369
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14982
- gi No. 1794147
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14983
- gi No. 2058706
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14984
- gi No. 2245093
- % Identity 74.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2393: from 1 to 113
- Alignment No. 14985
- gi No. 257238
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14986
- gi No. 267135
- % Identity 77.5
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111

- Alignment No. 14987
- gi No. 3264596
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14988
- gi No. 3298458
- % Identity 71.4
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2393: from 79 to 113
- Alignment No. 14989
- gi No. 461929
- % Identity 80.2
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2393: from 1 to 111
- Alignment No. 14990
- gi No. 4884870
- % Identity 75.4
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2393: from 45 to 113

Maximum Length Sequence corresponding to clone ID 314003

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2394
- Ceres seq\_id 1503322

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2395
- Ceres seq\_id 1503323
- Location of start within SEQ ID NO 2394: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2396
- Ceres seq\_id 1503324
- Location of start within SEQ ID NO 2394: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14991
- short chain dehydrogenase
- Location within SEQ ID NO 2396: from 7 to 102 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2397
- Ceres seq\_id 1503325
- Location of start within SEQ ID NO 2394: at 174 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 14992
- short chain dehydrogenase
- Location within SEQ ID NO 2397: from 1 to 96 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314019

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2398
- Ceres seq\_id 1503330

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2399
- Ceres seq\_id 1503331
- Location of start within SEQ ID NO 2398: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14993
- gi No. 4680192
- % Identity 87.4
- Alignment Length 143
- Location of Alignment in SEQ ID NO 2399: from 6 to 148

Maximum Length Sequence corresponding to clone ID 314030

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2400
- Ceres seq\_id 1503332

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2401
- Ceres seq\_id 1503333
- Location of start within SEQ ID NO 2400: at 132 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14994
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14995
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14996
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105
- Alignment No. 14997
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2401: from 1 to 105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2402
- Ceres seq\_id 1503334
- Location of start within SEQ ID NO 2400: at 156 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 14998
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2402: from 1 to 97
  
- Alignment No. 14999
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97
  
- Alignment No. 15000
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97
  
- Alignment No. 15001
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2402: from 1 to 97

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2403
- Ceres seq\_id 1503335
- Location of start within SEQ ID NO 2400: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15002
- gi No. 2997589
- % Identity 98.2
- Alignment Length 109
- Location of Alignment in SEQ ID NO 2403: from 1 to 88
  
- Alignment No. 15003
- gi No. 2997591
- % Identity 84.3
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88
  
- Alignment No. 15004
- gi No. 2997593
- % Identity 77.8
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88
  
- Alignment No. 15005
- gi No. 3367515
- % Identity 86.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2403: from 1 to 88

Maximum Length Sequence corresponding to clone ID 314034

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2404
- Ceres seq\_id 1503336

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2405
- Ceres seq\_id 1503337
- Location of start within SEQ ID NO 2404: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15006
- gi No. 4006906
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2405: from 2 to 13

Maximum Length Sequence corresponding to clone ID 314077

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2406
- Ceres seq\_id 1503342

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2407
- Ceres seq\_id 1503343
- Location of start within SEQ ID NO 2406: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15007
- gi No. 3786009
- % Identity 87.3
- Alignment Length 157
- Location of Alignment in SEQ ID NO 2407: from 1 to 157

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2408
- Ceres seq\_id 1503344
- Location of start within SEQ ID NO 2406: at 179 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15008
- gi No. 3786009
- % Identity 87.3
- Alignment Length 157
- Location of Alignment in SEQ ID NO 2408: from 1 to 98

Maximum Length Sequence corresponding to clone ID 314080

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2409
- Ceres seq\_id 1503345

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2410
- Ceres seq\_id 1503346
- Location of start within SEQ ID NO 2409: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2411
- Ceres seq\_id 1503347
- Location of start within SEQ ID NO 2409: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15009
- gi No. 2150000
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2411: from 1 to 53

Maximum Length Sequence corresponding to clone ID 314106

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2412
- Ceres seq\_id 1503351

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2413
- Ceres seq\_id 1503352
- Location of start within SEQ ID NO 2412: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15010
- gi No. 1185397
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15011
- gi No. 1644455
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15012
- gi No. 1644455
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15013
- gi No. 1644457
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15014
- gi No. 1644457
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15015
- gi No. 1644457
- % Identity 72.7
- Alignment Length 11



- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15016
- gi No. 1644457
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15017
- gi No. 1644459
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15018
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15019
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15020
- gi No. 1644459
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15021
- gi No. 1644461
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15022
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15023
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15024
- gi No. 1644461
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15025
- gi No. 178014
- % Identity 75
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2413: from 13 to 24

- Alignment No. 15026
  - gi No. 1914853
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15027
  - gi No. 19923
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15028
  - gi No. 2244878
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15029
  - gi No. 2462823
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15030
  - gi No. 322755
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 15 to 25
- Alignment No. 15031
  - gi No. 322755
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 15 to 25
- Alignment No. 15032
  - gi No. 322755
  - % Identity 71.4
  - Alignment Length 14
  - Location of Alignment in SEQ ID NO 2413: from 14 to 27
- Alignment No. 15033
  - gi No. 322757
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15034
  - gi No. 3551531
  - % Identity 81.8
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24
- Alignment No. 15035
  - gi No. 5306259
  - % Identity 72.7
  - Alignment Length 11
  - Location of Alignment in SEQ ID NO 2413: from 14 to 24

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2414
- Ceres seq\_id 1503353
- Location of start within SEQ ID NO 2412: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314122

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2415
- Ceres seq\_id 1503354

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2416
- Ceres seq\_id 1503355
- Location of start within SEQ ID NO 2415: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2417
- Ceres seq\_id 1503356
- Location of start within SEQ ID NO 2415: at 9 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2418
- Ceres seq\_id 1503357
- Location of start within SEQ ID NO 2415: at 103 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15036
- DnaJ domain
- Location within SEQ ID NO 2418: from 24 to 75 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314197

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2419
- Ceres seq\_id 1503378

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2420
- Ceres seq\_id 1503379
- Location of start within SEQ ID NO 2419: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15037
- Protein phosphatase 2C
- Location within SEQ ID NO 2420: from 3 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314305

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2421
- Ceres seq\_id 1503400

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2422
- Ceres seq\_id 1503401
- Location of start within SEQ ID NO 2421: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15038
- gi No. 445612
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2422: from 39 to 81

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2423
- Ceres seq\_id 1503402
- Location of start within SEQ ID NO 2421: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2424
- Ceres seq\_id 1503403
- Location of start within SEQ ID NO 2421: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15039
- gi No. 445612
- % Identity 72.1
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2424: from 6 to 48

Maximum Length Sequence corresponding to clone ID 314409

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2425
- Ceres seq\_id 1503422

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2426
- Ceres seq\_id 1503423
- Location of start within SEQ ID NO 2425: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15040
- gi No. 1743388
- % Identity 94.2
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2426: from 77 to 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2427

- Ceres seq\_id 1503424
- Location of start within SEQ ID NO 2425: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15041
  - gi No. 1743388
  - % Identity 94.2
  - Alignment Length 86
  - Location of Alignment in SEQ ID NO 2427: from 33 to 117

Maximum Length Sequence corresponding to clone ID 314420

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2428
- Ceres seq\_id 1503429

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2429
- Ceres seq\_id 1503430
- Location of start within SEQ ID NO 2428: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15042
  - gi No. 2914700
  - % Identity 86.7
  - Alignment Length 30
  - Location of Alignment in SEQ ID NO 2429: from 2 to 31

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2430
- Ceres seq\_id 1503431
- Location of start within SEQ ID NO 2428: at 183 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2431
- Ceres seq\_id 1503432
- Location of start within SEQ ID NO 2428: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314461

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2432
- Ceres seq\_id 1503443

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2433
- Ceres seq\_id 1503444
- Location of start within SEQ ID NO 2432: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2434
- Ceres seq\_id 1503445
- Location of start within SEQ ID NO 2432: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15043
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2434: from 38 to 51
- Alignment No. 15044
- gi No. 4008584
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2434: from 41 to 51
- Alignment No. 15045
- gi No. 4008584
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2434: from 37 to 51
- Alignment No. 15046
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2434: from 38 to 51
- Alignment No. 15047
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2434: from 38 to 51
- Alignment No. 15048
- gi No. 688080
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2434: from 42 to 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2435
- Ceres seq\_id 1503446
- Location of start within SEQ ID NO 2432: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15049
- gi No. 119111
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
- Alignment No. 15050
- gi No. 4008584
- % Identity 75

- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 8 to 18
- Alignment No. 15051
- gi No. 4008584
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2435: from 4 to 18
- Alignment No. 15052
- gi No. 628112
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
- Alignment No. 15053
- gi No. 628185
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2435: from 5 to 18
- Alignment No. 15054
- gi No. 688080
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2435: from 9 to 19

Maximum Length Sequence corresponding to clone ID 314605

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2436
- Ceres seq\_id 1503476

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2437
- Ceres seq\_id 1503477
- Location of start within SEQ ID NO 2436: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2438
- Ceres seq\_id 1503478
- Location of start within SEQ ID NO 2436: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15055
- Chitin recognition protein
- Location within SEQ ID NO 2438: from 44 to 77 aa.
- Alignment No. 15056
- Chitinases class I
- Location within SEQ ID NO 2438: from 90 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15057
- gi No. 299189
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2438: from 49 to 69

- Alignment No. 15058
- gi No. 299190
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2438: from 49 to 69
- Alignment No. 15059
- gi No. 994881
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2438: from 112 to 144

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2439
- Ceres seq\_id 1503479
- Location of start within SEQ ID NO 2436: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15060
- Chitin recognition protein
- Location within SEQ ID NO 2439: from 25 to 58 aa.
- Alignment No. 15061
- Chitinases class I
- Location within SEQ ID NO 2439: from 71 to 127 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15062
- gi No. 299189
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2439: from 30 to 50
- Alignment No. 15063
- gi No. 299190
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2439: from 30 to 50
- Alignment No. 15064
- gi No. 994881
- % Identity 75.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2439: from 93 to 125

Maximum Length Sequence corresponding to clone ID 314613

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2440
- Ceres seq\_id 1503480

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2441
- Ceres seq\_id 1503481
- Location of start within SEQ ID NO 2440: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15065
- chorismate binding enzyme
- Location within SEQ ID NO 2441: from 4 to 147 aa.



(D) Related Amino Acid Sequences

- Alignment No. 15066
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15067
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2441: from 2 to 147
  
- Alignment No. 15068
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2441: from 2 to 155
  
- Alignment No. 15069
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15070
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2441: from 2 to 147
  
- Alignment No. 15071
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15072
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2441: from 1 to 147
  
- Alignment No. 15073
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2441: from 4 to 147
  
- Alignment No. 15074
- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2441: from 1 to 147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2442
- Ceres seq\_id 1503482
- Location of start within SEQ ID NO 2440: at 4 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15075
- chorismate binding enzyme
- Location within SEQ ID NO 2442: from 3 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15076
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15077
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15078
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2442: from 1 to 154
- Alignment No. 15079
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15080
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15081
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15082
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2442: from 1 to 146
- Alignment No. 15083
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2442: from 3 to 146
- Alignment No. 15084
- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2442: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2443
- Ceres seq\_id 1503483
- Location of start within SEQ ID NO 2440: at 55 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15085
- chorismate binding enzyme
- Location within SEQ ID NO 2443: from 1 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15086
- gi No. 320552
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15087
- gi No. 320553
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15088
- gi No. 3348124
- % Identity 76.8
- Alignment Length 155
- Location of Alignment in SEQ ID NO 2443: from 1 to 137
- Alignment No. 15089
- gi No. 418133
- % Identity 82.6
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15090
- gi No. 418134
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15091
- gi No. 5360657
- % Identity 78.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15092
- gi No. 5360659
- % Identity 95.2
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15093
- gi No. 960289
- % Identity 83.3
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2443: from 1 to 129
- Alignment No. 15094

- gi No. 960291
- % Identity 80.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2443: from 1 to 129

Maximum Length Sequence corresponding to clone ID 314618

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2444
- Ceres seq\_id 1503484

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2445
- Ceres seq\_id 1503485
- Location of start within SEQ ID NO 2444: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15095
- Thioredoxin
- Location within SEQ ID NO 2445: from 22 to 128 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15096
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2445: from 16 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2446
- Ceres seq\_id 1503486
- Location of start within SEQ ID NO 2444: at 46 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15097
- Thioredoxin
- Location within SEQ ID NO 2446: from 7 to 113 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15098
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2446: from 1 to 123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2447
- Ceres seq\_id 1503487
- Location of start within SEQ ID NO 2444: at 109 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15099
- Thioredoxin
- Location within SEQ ID NO 2447: from 1 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15100
- gi No. 3915131
- % Identity 70.7
- Alignment Length 123

- Location of Alignment in SEQ ID NO 2447: from 1 to 102

Maximum Length Sequence corresponding to clone ID 314637

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2448
- Ceres seq\_id 1503492

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2449
- Ceres seq\_id 1503493
- Location of start within SEQ ID NO 2448: at 201 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 15101
- Chalcone and stilbene synthases
- Location within SEQ ID NO 2449: from 12 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15102
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2449: from 41 to 62

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2450
- Ceres seq\_id 1503494
- Location of start within SEQ ID NO 2448: at 228 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 15103
- Chalcone and stilbene synthases
- Location within SEQ ID NO 2450: from 3 to 53 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15104
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2450: from 32 to 53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2451
- Ceres seq\_id 1503495
- Location of start within SEQ ID NO 2448: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15105
- gi No. 322636
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2451: from 21 to 42

Maximum Length Sequence corresponding to clone ID 314643

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2452
- Ceres seq\_id 1503496

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2453
- Ceres seq\_id 1503497
- Location of start within SEQ ID NO 2452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15106
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2453: from 9 to 136 aa.
- Alignment No. 15107
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2453: from 28 to 151 aa.
- Alignment No. 15108
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2453: from 23 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2454
- Ceres seq\_id 1503498
- Location of start within SEQ ID NO 2452: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15109
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2454: from 9 to 136 aa.
- Alignment No. 15110
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2454: from 28 to 151 aa.
- Alignment No. 15111
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2454: from 23 to 125 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2455
- Ceres seq\_id 1503499
- Location of start within SEQ ID NO 2452: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314669

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2456
- Ceres seq\_id 1503507

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2457
- Ceres seq\_id 1503508
- Location of start within SEQ ID NO 2456: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15112
  - gi No. 2894378
  - % Identity 82.5
  - Alignment Length 114
  - Location of Alignment in SEQ ID NO 2457: from 1 to 114

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2458
  - Ceres seq\_id 1503509
  - Location of start within SEQ ID NO 2456: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15113
  - gi No. 2894378
  - % Identity 82.5
  - Alignment Length 114
  - Location of Alignment in SEQ ID NO 2458: from 1 to 38

Maximum Length Sequence corresponding to clone ID 314683

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2459
  - Ceres seq\_id 1503510
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2460
  - Ceres seq\_id 1503511
  - Location of start within SEQ ID NO 2459: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15114
  - gi No. 4091080
  - % Identity 70.7
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 2460: from 1 to 57

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2461
  - Ceres seq\_id 1503512
  - Location of start within SEQ ID NO 2459: at 39 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15115
  - gi No. 4091080
  - % Identity 70.7
  - Alignment Length 59
  - Location of Alignment in SEQ ID NO 2461: from 1 to 45

Maximum Length Sequence corresponding to clone ID 314729

- (A) Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 2462
  - Ceres seq\_id 1503522
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 2463
  - Ceres seq\_id 1503523
  - Location of start within SEQ ID NO 2462: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15116
- gi No. 1173045
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15117
- gi No. 1346945
- % Identity 78.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15118
- gi No. 2281793
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2463: from 12 to 28
  
- Alignment No. 15119
- gi No. 2565332
- % Identity 73.1
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2463: from 3 to 28
  
- Alignment No. 15120
- gi No. 2996185
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15121
- gi No. 3098458
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2463: from 1 to 28
  
- Alignment No. 15122
- gi No. 3845189
- % Identity 73.9
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15123
- gi No. 400996
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15124
- gi No. 4090257
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
  
- Alignment No. 15125
- gi No. 4455775
- % Identity 71.4



- Alignment Length 28
- Location of Alignment in SEQ ID NO 2463: from 1 to 28
- Alignment No. 15126
- gi No. 4506643
- % Identity 91.3
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15127
- gi No. 4741896
- % Identity 100
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2463: from 1 to 23
- Alignment No. 15128
- gi No. 5007072
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2463: from 9 to 23

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2464
- Ceres seq\_id 1503524
- Location of start within SEQ ID NO 2462: at 127 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2465
- Ceres seq\_id 1503525
- Location of start within SEQ ID NO 2462: at 139 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314734

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2466
- Ceres seq\_id 1503526

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2467
- Ceres seq\_id 1503527
- Location of start within SEQ ID NO 2466: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2468
- Ceres seq\_id 1503528
- Location of start within SEQ ID NO 2466: at 162 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15129
- Ribosomal protein L13

- Location within SEQ ID NO 2468: from 29 to 85 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2469
- Ceres seq\_id 1503529
- Location of start within SEQ ID NO 2466: at 352 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314824

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2470
- Ceres seq\_id 1503550

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2471
- Ceres seq\_id 1503551
- Location of start within SEQ ID NO 2470: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15130
- gi No. 3935157
- % Identity 71.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2471: from 28 to 150

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2472
- Ceres seq\_id 1503552
- Location of start within SEQ ID NO 2470: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2473
- Ceres seq\_id 1503553
- Location of start within SEQ ID NO 2470: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15131
- gi No. 3935157
- % Identity 71.5
- Alignment Length 123
- Location of Alignment in SEQ ID NO 2473: from 4 to 126

Maximum Length Sequence corresponding to clone ID 314826

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2474
- Ceres seq\_id 1503554

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2475
- Ceres seq\_id 1503555

- Location of start within SEQ ID NO 2474: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15132
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2475: from 2 to 94 aa.
- Alignment No. 15133
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2475: from 9 to 133 aa.
- Alignment No. 15134
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2475: from 11 to 138 aa.
- Alignment No. 15135
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2475: from 3 to 114 aa.
- Alignment No. 15136
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2475: from 4 to 138 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15137
- gi No. 2281102
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2475: from 128 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2476
- Ceres seq\_id 1503556
- Location of start within SEQ ID NO 2474: at 60 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15138
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2476: from 1 to 75 aa.
- Alignment No. 15139
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2476: from 1 to 114 aa.
- Alignment No. 15140
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2476: from 1 to 119 aa.
- Alignment No. 15141
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2476: from 1 to 95 aa.
- Alignment No. 15142
- Assemblin (Peptidase family S21)
- Location within SEQ ID NO 2476: from 1 to 119 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15143
- gi No. 2281102

- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2476: from 109 to 119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2477
- Ceres seq\_id 1503557
- Location of start within SEQ ID NO 2474: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15144
- gi No. 109944
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15145
- gi No. 1350911
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15146
- gi No. 1350912
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15147
- gi No. 200880
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15148
- gi No. 2564955
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2477: from 76 to 86
  
- Alignment No. 15149
- gi No. 337720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15150
- gi No. 483195
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87
  
- Alignment No. 15151
- gi No. 542994
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2477: from 74 to 87

Maximum Length Sequence corresponding to clone ID 314875

- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2478  
- Ceres seq\_id 1503569
- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2479  
- Ceres seq\_id 1503570  
- Location of start within SEQ ID NO 2478: at 1 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences  
- Alignment No. 15152  
- gi No. 4455361  
- % Identity 72.2  
- Alignment Length 54  
- Location of Alignment in SEQ ID NO 2479: from 34 to 87
- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2480  
- Ceres seq\_id 1503571  
- Location of start within SEQ ID NO 2478: at 100 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences  
- Alignment No. 15153  
- gi No. 4455361  
- % Identity 72.2  
- Alignment Length 54  
- Location of Alignment in SEQ ID NO 2480: from 1 to 54
- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2481  
- Ceres seq\_id 1503572  
- Location of start within SEQ ID NO 2478: at 142 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (D) Related Amino Acid Sequences  
- Alignment No. 15154  
- gi No. 4455361  
- % Identity 72.2  
- Alignment Length 54  
- Location of Alignment in SEQ ID NO 2481: from 1 to 40
- Maximum Length Sequence corresponding to clone ID 314917
- (A) Polynucleotide Sequence  
- Pat. Appln. SEQ ID NO 2482  
- Ceres seq\_id 1503585
- (B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2483  
- Ceres seq\_id 1503586  
- Location of start within SEQ ID NO 2482: at 87 nt.
- (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)  
- Alignment No. 15155  
- WD domain, G-beta repeat  
- Location within SEQ ID NO 2483: from 20 to 58 aa.
- (D) Related Amino Acid Sequences

- ```
- Alignment No. 15156
- gi No. 1143814
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15157
- gi No. 1346106
- % Identity 74.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15158
- gi No. 1346107
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15159
- gi No. 2935698
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15160
- gi No. 3023832
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15161
- gi No. 3023839
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15162
- gi No. 3023841
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15163
- gi No. 3023842
- % Identity 75.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15164
- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15165
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

- Alignment No. 15166
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- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2483: from 1 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2484
- Ceres seq\_id 1503587
- Location of start within SEQ ID NO 2482: at 261 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15167
- gi No. 1143814
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15168
- gi No. 1346106
- % Identity 74.8
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15169
- gi No. 1346107
- % Identity 99.1
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15170
- gi No. 2935698
- % Identity 91.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15171
- gi No. 3023832
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15172
- gi No. 3023839
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15173
- gi No. 3023841
- % Identity 73
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
  
- Alignment No. 15174
- gi No. 3023842
- % Identity 75.7
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

- Alignment No. 15175
- gi No. 3023843
- % Identity 92.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
- Alignment No. 15176
- gi No. 3023859
- % Identity 74.8
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50
- Alignment No. 15177
- gi No. 4929352
- % Identity 76.6
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2484: from 1 to 50

Maximum Length Sequence corresponding to clone ID 314924

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2485
- Ceres seq\_id 1503588

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2486
- Ceres seq\_id 1503589
- Location of start within SEQ ID NO 2485: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15178
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2486: from 1 to 100 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15179
- gi No. 1142614
- % Identity 85.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15180
- gi No. 1174848
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 98
- Alignment No. 15181
- gi No. 1174849
- % Identity 79.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15182
- gi No. 136643
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15183
- gi No. 136645
- % Identity 75.7



- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15184
- gi No. 136646
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15185
- gi No. 2130087
- % Identity 81.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15186
- gi No. 2130088
- % Identity 80.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15187
- gi No. 2136339
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15188
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15189
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 1 to 74
- Alignment No. 15190
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15191
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2486: from 59 to 100
- Alignment No. 15192
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15193
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105

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- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15194
- gi No. 4097684
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 12 to 100
- Alignment No. 15195
- gi No. 4100646
- % Identity 81.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15196
- gi No. 441457
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15197
- gi No. 4433363
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2486: from 32 to 100
- Alignment No. 15198
- gi No. 4507773
- % Identity 74.8
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15199
- gi No. 4507775
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15200
- gi No. 4507777
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15201
- gi No. 456568
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15202
- gi No. 4581117
- % Identity 85.2
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15203
- gi No. 4583656
- % Identity 73.9
- Alignment Length 111
- Location of Alignment in SEQ ID NO 2486: from 1 to 98

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- Alignment No. 15204
- gi No. 464979
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15205
- gi No. 464981
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15206
- gi No. 464985
- % Identity 87.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15207
- gi No. 464986
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15208
- gi No. 464987
- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15209
- gi No. 464988
- % Identity 91.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2486: from 2 to 100
- Alignment No. 15210
- gi No. 477134
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15211
- gi No. 4868140
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2486: from 1 to 100
- Alignment No. 15212
- gi No. 4868141
- % Identity 79.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2486: from 12 to 100

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2487
- Ceres seq\_id 1503590
- Location of start within SEQ ID NO 2485: at 208 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 15213
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2487: from 1 to 92 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15214
- gi No. 1142614
- % Identity 85.2
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15215
- gi No. 1174848
- % Identity 76.1
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 90
- Alignment No. 15216
- gi No. 1174849
- % Identity 79.6
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15217
- gi No. 136643
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15218
- gi No. 136645
- % Identity 75.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15219
- gi No. 136646
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15220
- gi No. 2130087
- % Identity 81.4
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15221
- gi No. 2130088
- % Identity 80.5
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15222
- gi No. 2136339
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15223
- gi No. 2501431
- % Identity 75.2
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15224
- gi No. 2612962
- % Identity 75.3
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 1 to 66
- Alignment No. 15225
- gi No. 2668744
- % Identity 90.3
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15226
- gi No. 3043432
- % Identity 95.2
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2487: from 51 to 92
- Alignment No. 15227
- gi No. 3323498
- % Identity 77.4
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15228
- gi No. 3915190
- % Identity 93.3
- Alignment Length 105
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15229
- gi No. 4097684
- % Identity 82
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92
- Alignment No. 15230
- gi No. 4100646
- % Identity 81.7
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15231
- gi No. 441457
- % Identity 88.5
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15232
- gi No. 4433363
- % Identity 94.2
- Alignment Length 69
- Location of Alignment in SEQ ID NO 2487: from 24 to 92
- Alignment No. 15233

- gi No. 4507773  
- % Identity 74.8  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15234  
- gi No. 4507775  
- % Identity 78.3  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15235  
- gi No. 4507777  
- % Identity 78.3  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15236  
- gi No. 456568  
- % Identity 88.5  
- Alignment Length 113  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15237  
- gi No. 4581117  
- % Identity 85.2  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15238  
- gi No. 4583656  
- % Identity 73.9  
- Alignment Length 111  
- Location of Alignment in SEQ ID NO 2487: from 1 to 90

- Alignment No. 15239  
- gi No. 464979  
- % Identity 76.5  
- Alignment Length 115  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15240  
- gi No. 464981  
- % Identity 89.4  
- Alignment Length 113  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15241  
- gi No. 464985  
- % Identity 87.6  
- Alignment Length 113  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15242  
- gi No. 464986  
- % Identity 89.4  
- Alignment Length 113  
- Location of Alignment in SEQ ID NO 2487: from 1 to 92

- Alignment No. 15243  
- gi No. 464987

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- % Identity 89.4
- Alignment Length 113
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15244
- gi No. 464988
- % Identity 91.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15245
- gi No. 477134
- % Identity 76.5
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15246
- gi No. 4868140
- % Identity 78.3
- Alignment Length 115
- Location of Alignment in SEQ ID NO 2487: from 1 to 92
- Alignment No. 15247
- gi No. 4868141
- % Identity 79.8
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2487: from 4 to 92

Maximum Length Sequence corresponding to clone ID 314967

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2488
- Ceres seq\_id 1503591

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2489
- Ceres seq\_id 1503592
- Location of start within SEQ ID NO 2488: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15248
- Glycosyl hydrolases family 16
- Location within SEQ ID NO 2489: from 1 to 115 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15249
- gi No. 2129770
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126
- Alignment No. 15250
- gi No. 2154609
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126
- Alignment No. 15251
- gi No. 5533313
- % Identity 70.9
- Alignment Length 127
- Location of Alignment in SEQ ID NO 2489: from 1 to 126

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2490
- Ceres seq\_id 1503593
- Location of start within SEQ ID NO 2488: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15252
- Mucin-like glycoprotein
- Location within SEQ ID NO 2490: from 1 to 126 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314971

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2491
- Ceres seq\_id 1503594

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2492
- Ceres seq\_id 1503595
- Location of start within SEQ ID NO 2491: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15253
- Ubiquitin-conjugating enzyme
- Location within SEQ ID NO 2492: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15254
- gi No. 4006890
- % Identity 84.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2492: from 1 to 59
- Alignment No. 15255
- gi No. 4217999
- % Identity 84.7
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2492: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2493
- Ceres seq\_id 1503596
- Location of start within SEQ ID NO 2491: at 224 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2494
- Ceres seq\_id 1503597
- Location of start within SEQ ID NO 2491: at 246 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 314996



(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2495
- Ceres seq\_id 1503600

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2496
- Ceres seq\_id 1503601
- Location of start within SEQ ID NO 2495: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15256
- gi No. 1173018
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15257
- gi No. 132849
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15258
- gi No. 266944
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15259
- gi No. 2961372
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15260
- gi No. 3088346
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49
- Alignment No. 15261
- gi No. 4406816
- % Identity 100
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2496: from 35 to 49

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2497
- Ceres seq\_id 1503602
- Location of start within SEQ ID NO 2495: at 79 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15262
- Ribosomal Proteins L2
- Location within SEQ ID NO 2497: from 25 to 110 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15263
- gi No. 132849

- % Identity 75.9
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
- Alignment No. 15264
- gi No. 266944
- % Identity 77.7
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
- Alignment No. 15265
- gi No. 2961372
- % Identity 74.1
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110
- Alignment No. 15266
- gi No. 4406816
- % Identity 75
- Alignment Length 112
- Location of Alignment in SEQ ID NO 2497: from 1 to 110

Maximum Length Sequence corresponding to clone ID 315057

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2498
- Ceres seq\_id 1503615

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2499
- Ceres seq\_id 1503616
- Location of start within SEQ ID NO 2498: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15267
- gi No. 481728
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2499: from 76 to 86
- Alignment No. 15268
- gi No. 481728
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2499: from 76 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2500
- Ceres seq\_id 1503617
- Location of start within SEQ ID NO 2498: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15269
- gi No. 3941736
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
- Alignment No. 15270

- gi No. 4337109
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
- Alignment No. 15271
- gi No. 4758110
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
- Alignment No. 15272
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 93 to 104
- Alignment No. 15273
- gi No. 5668598
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2500: from 95 to 106

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2501
- Ceres seq\_id 1503618
- Location of start within SEQ ID NO 2498: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315079

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2502
- Ceres seq\_id 1503621

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2503
- Ceres seq\_id 1503622
- Location of start within SEQ ID NO 2502: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15274
- Putative GTP-ase activating protein for Arf
- Location within SEQ ID NO 2503: from 74 to 132 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15275
- gi No. 3236238
- % Identity 83.1
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2503: from 74 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2504
- Ceres seq\_id 1503623
- Location of start within SEQ ID NO 2502: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2505
- Ceres seq\_id 1503624
- Location of start within SEQ ID NO 2502: at 140 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315215

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2506
- Ceres seq\_id 1503662

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2507
- Ceres seq\_id 1503663
- Location of start within SEQ ID NO 2506: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15276
- gi No. 3123264
- % Identity 75.5
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2507: from 81 to 128

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2508
- Ceres seq\_id 1503664
- Location of start within SEQ ID NO 2506: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15277
- gi No. 3123264
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2508: from 26 to 86
- Alignment No. 15278
- gi No. 498906
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2508: from 26 to 86
- Alignment No. 15279
- gi No. 730547
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2508: from 26 to 86

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2509
- Ceres seq\_id 1503665
- Location of start within SEQ ID NO 2506: at 78 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15280
- gi No. 3123264
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61
  
- Alignment No. 15281
- gi No. 498906
- % Identity 70.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61
  
- Alignment No. 15282
- gi No. 730547
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2509: from 1 to 61

Maximum Length Sequence corresponding to clone ID 315227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2510
- Ceres seq\_id 1503670

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2511
- Ceres seq\_id 1503671
- Location of start within SEQ ID NO 2510: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15283
- gi No. 1170395
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
  
- Alignment No. 15284
- gi No. 1170396
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
  
- Alignment No. 15285
- gi No. 1170396
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2511: from 29 to 45
  
- Alignment No. 15286
- gi No. 1170397
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
  
- Alignment No. 15287
- gi No. 1170397
- % Identity 70.6
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2511: from 29 to 45
- Alignment No. 15288
- gi No. 1170398
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2511: from 29 to 43
- Alignment No. 15289
- gi No. 1170398
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2511: from 29 to 45

Maximum Length Sequence corresponding to clone ID 315373

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2512
- Ceres seq\_id 1503697

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2513
- Ceres seq\_id 1503698
- Location of start within SEQ ID NO 2512: at 73 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 15290
- Copper amine oxidase
- Location within SEQ ID NO 2513: from 1 to 123 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15291
- gi No. 4559342
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122
- Alignment No. 15292
- gi No. 4567319
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122
- Alignment No. 15293
- gi No. 5230728
- % Identity 90.8
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2513: from 1 to 122

Maximum Length Sequence corresponding to clone ID 315404

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2514
- Ceres seq\_id 1503703

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2515
- Ceres seq\_id 1503704
- Location of start within SEQ ID NO 2514: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2516
- Ceres seq\_id 1503705
- Location of start within SEQ ID NO 2514: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15294
- gi No. 4512664
- % Identity 77.8
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2516: from 35 to 79
- Alignment No. 15295
- gi No. 4874278
- % Identity 74
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15296
- gi No. 4902470
- % Identity 74
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15297
- gi No. 4902877
- % Identity 72.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2516: from 75 to 151
- Alignment No. 15298
- gi No. 4902879
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2516: from 36 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2517
- Ceres seq\_id 1503706
- Location of start within SEQ ID NO 2514: at 72 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15299
- gi No. 4512664
- % Identity 77.8
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2517: from 12 to 56
- Alignment No. 15300
- gi No. 4874278
- % Identity 74
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15301
- gi No. 4902470
- % Identity 74

- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15302
- gi No. 4902877
- % Identity 72.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2517: from 52 to 128
- Alignment No. 15303
- gi No. 4902879
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2517: from 13 to 56

Maximum Length Sequence corresponding to clone ID 315430

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2518
- Ceres seq\_id 1503714

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2519
- Ceres seq\_id 1503715
- Location of start within SEQ ID NO 2518: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15304
- 7 transmembrane receptor (rhodopsin family)
- Location within SEQ ID NO 2519: from 36 to 129 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15305
- gi No. 141279
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2519: from 46 to 62
- Alignment No. 15306
- gi No. 1914851
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2519: from 46 to 61
- Alignment No. 15307
- gi No. 2224619
- % Identity 70
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2519: from 49 to 68
- Alignment No. 15308
- gi No. 539033
- % Identity 72
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2519: from 46 to 70
- Alignment No. 15309
- gi No. 688080
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2519: from 48 to 60



- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2520
  - Ceres seq\_id 1503716
  - Location of start within SEQ ID NO 2518: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2521
  - Ceres seq\_id 1503717
  - Location of start within SEQ ID NO 2518: at 65 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315437

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2522
  - Ceres seq\_id 1503718

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2523
  - Ceres seq\_id 1503719
  - Location of start within SEQ ID NO 2522: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15310
- Cystatin domain
- Location within SEQ ID NO 2523: from 77 to 132 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315445

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2524
  - Ceres seq\_id 1503720

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2525
  - Ceres seq\_id 1503721
  - Location of start within SEQ ID NO 2524: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2526
  - Ceres seq\_id 1503722
  - Location of start within SEQ ID NO 2524: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2527
  - Ceres seq\_id 1503723
  - Location of start within SEQ ID NO 2524: at 200 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15311
- Armadillo/beta-catenin-like repeats
- Location within SEQ ID NO 2527: from 21 to 62 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15312
- gi No. 2950210
- % Identity 73
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2527: from 21 to 93
- Alignment No. 15313
- gi No. 3091280
- % Identity 70.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2527: from 22 to 77
- Alignment No. 15314
- gi No. 3122278
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2527: from 22 to 77
- Alignment No. 15315
- gi No. 3273243
- % Identity 71.6
- Alignment Length 74
- Location of Alignment in SEQ ID NO 2527: from 21 to 93

Maximum Length Sequence corresponding to clone ID 315466

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2528
- Ceres seq\_id 1503728

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2529
- Ceres seq\_id 1503729
- Location of start within SEQ ID NO 2528: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15316
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2529: from 4 to 108 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315475

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2530
- Ceres seq\_id 1503734

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2531
- Ceres seq\_id 1503735
- Location of start within SEQ ID NO 2530: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15317

- Multicopper oxidase
- Location within SEQ ID NO 2531: from 22 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15318
- gi No. 4454012
- % Identity 71.6
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2531: from 23 to 110
- Alignment No. 15319
- gi No. 4725941
- % Identity 71.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2531: from 22 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2532
- Ceres seq\_id 1503736
- Location of start within SEQ ID NO 2530: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2533
- Ceres seq\_id 1503737
- Location of start within SEQ ID NO 2530: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15320
- Multicopper oxidase
- Location within SEQ ID NO 2533: from 6 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15321
- gi No. 4454012
- % Identity 71.6
- Alignment Length 88
- Location of Alignment in SEQ ID NO 2533: from 7 to 94
- Alignment No. 15322
- gi No. 4725941
- % Identity 71.9
- Alignment Length 89
- Location of Alignment in SEQ ID NO 2533: from 6 to 94

Maximum Length Sequence corresponding to clone ID 315510

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2534
- Ceres seq\_id 1503743

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2535
- Ceres seq\_id 1503744
- Location of start within SEQ ID NO 2534: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2536
- Ceres seq\_id 1503745
- Location of start within SEQ ID NO 2534: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15323
- gi No. 1076556
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2536: from 20 to 31
- Alignment No. 15324
- gi No. 1655699
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2536: from 18 to 29
- Alignment No. 15325
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15326
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15327
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15328
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15329
- gi No. 1655699
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15330
- gi No. 1655699
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15331
- gi No. 1655699
- % Identity 70.6
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2536: from 17 to 32
- Alignment No. 15332
- gi No. 322747
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30
- Alignment No. 15333
- gi No. 322749
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2536: from 17 to 30

Maximum Length Sequence corresponding to clone ID 315548

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2537
- Ceres seq\_id 1503746

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2538
- Ceres seq\_id 1503747
- Location of start within SEQ ID NO 2537: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2539
- Ceres seq\_id 1503748
- Location of start within SEQ ID NO 2537: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15334
- gi No. 112110
- % Identity 74.1
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2539: from 2 to 28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2540
- Ceres seq\_id 1503749
- Location of start within SEQ ID NO 2537: at 301 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315587

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2541
- Ceres seq\_id 1503769

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2542
- Ceres seq\_id 1503770
- Location of start within SEQ ID NO 2541: at 104 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 15335
- Nucleoside diphosphate kinases
- Location within SEQ ID NO 2542: from 2 to 114 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15336
- gi No. 1076713
- % Identity 87
- Alignment Length 23
- Location of Alignment in SEQ ID NO 2542: from 1 to 22
  
- Alignment No. 15337
- gi No. 1304478
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2542: from 2 to 38
  
- Alignment No. 15338
- gi No. 1729427
- % Identity 71.1
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2542: from 1 to 38
  
- Alignment No. 15339
- gi No. 2129487
- % Identity 80.2
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114
  
- Alignment No. 15340
- gi No. 2829275
- % Identity 88.8
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114
  
- Alignment No. 15341
- gi No. 4972094
- % Identity 90.5
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2542: from 1 to 114

Maximum Length Sequence corresponding to clone ID 315593

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2543
- Ceres seq\_id 1503775

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2544
- Ceres seq\_id 1503776
- Location of start within SEQ ID NO 2543: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15342
- Elongation factor G C-terminus
- Location within SEQ ID NO 2544: from 21 to 152 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15343
- gi No. 4895248
- % Identity 83.3
- Alignment Length 156

- Location of Alignment in SEQ ID NO 2544: from 1 to 156

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2545
- Ceres seq\_id 1503777
- Location of start within SEQ ID NO 2543: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15344
- Elongation factor G C-terminus
- Location within SEQ ID NO 2545: from 1 to 116 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15345
- gi No. 4895248
- % Identity 83.3
- Alignment Length 156
- Location of Alignment in SEQ ID NO 2545: from 1 to 120

Maximum Length Sequence corresponding to clone ID 315595

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2546
- Ceres seq\_id 1503778

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2547
- Ceres seq\_id 1503779
- Location of start within SEQ ID NO 2546: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15346
- gi No. 3786005
- % Identity 80.8
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2547: from 1 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2548
- Ceres seq\_id 1503780
- Location of start within SEQ ID NO 2546: at 269 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2549
- Ceres seq\_id 1503781
- Location of start within SEQ ID NO 2546: at 324 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315627

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2550
- Ceres seq\_id 1503796

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2551
- Ceres seq\_id 1503797
- Location of start within SEQ ID NO 2550: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2552
- Ceres seq\_id 1503798
- Location of start within SEQ ID NO 2550: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15347
- gi No. 2352921
- % Identity 87.1
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38
- Alignment No. 15348
- gi No. 2352923
- % Identity 82.3
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38
- Alignment No. 15349
- gi No. 3021508
- % Identity 73.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
- Alignment No. 15350
- gi No. 3021510
- % Identity 76.1
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
- Alignment No. 15351
- gi No. 3023815
- % Identity 77.4
- Alignment Length 62
- Location of Alignment in SEQ ID NO 2552: from 1 to 38
- Alignment No. 15352
- gi No. 4206114
- % Identity 77.6
- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
- Alignment No. 15353
- gi No. 5360754
- % Identity 87.5
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2552: from 1 to 41
- Alignment No. 15354
- gi No. 585165
- % Identity 76.1



- Alignment Length 67
- Location of Alignment in SEQ ID NO 2552: from 1 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2553
- Ceres seq\_id 1503799
- Location of start within SEQ ID NO 2550: at 262 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15355
- Glucose-6-phosphate dehydrogenase
- Location within SEQ ID NO 2553: from 1 to 42 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15356
- gi No. 1169799
- % Identity 70.7
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2553: from 3 to 43
- Alignment No. 15357
- gi No. 3021508
- % Identity 81
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2553: from 3 to 43
- Alignment No. 15358
- gi No. 585165
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2553: from 1 to 43

Maximum Length Sequence corresponding to clone ID 315647

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2554
- Ceres seq\_id 1503810

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2555
- Ceres seq\_id 1503811
- Location of start within SEQ ID NO 2554: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15359
- gi No. 1173201
- % Identity 75.7
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2555: from 37 to 73
- Alignment No. 15360
- gi No. 131772
- % Identity 97.6
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15361
- gi No. 131773
- % Identity 89.7
- Alignment Length 39

- Location of Alignment in SEQ ID NO 2555: from 35 to 73
- Alignment No. 15362
- gi No. 133720
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2555: from 60 to 73
- Alignment No. 15363
- gi No. 2350992
- % Identity 80
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2555: from 59 to 73
- Alignment No. 15364
- gi No. 2414647
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2555: from 48 to 73
- Alignment No. 15365
- gi No. 3097244
- % Identity 71.4
- Alignment Length 42
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15366
- gi No. 3122785
- % Identity 78
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15367
- gi No. 4574240
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2555: from 53 to 73
- Alignment No. 15368
- gi No. 4678226
- % Identity 80.5
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73
- Alignment No. 15369
- gi No. 4886269
- % Identity 82.9
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2555: from 33 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2556
- Ceres seq\_id 1503812
- Location of start within SEQ ID NO 2554: at 99 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15370
- gi No. 1173201
- % Identity 75.7

- Alignment Length 37  
- Location of Alignment in SEQ ID NO 2556: from 5 to 41

- Alignment No. 15371  
- gi No. 131772  
- % Identity 97.6  
- Alignment Length 41  
- Location of Alignment in SEQ ID NO 2556: from 1 to 41

- Alignment No. 15372  
- gi No. 131773  
- % Identity 89.7  
- Alignment Length 39  
- Location of Alignment in SEQ ID NO 2556: from 3 to 41

- Alignment No. 15373  
- gi No. 133720  
- % Identity 71.4  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2556: from 28 to 41

- Alignment No. 15374  
- gi No. 2350992  
- % Identity 80  
- Alignment Length 15  
- Location of Alignment in SEQ ID NO 2556: from 27 to 41

- Alignment No. 15375  
- gi No. 2414647  
- % Identity 76.9  
- Alignment Length 26  
- Location of Alignment in SEQ ID NO 2556: from 16 to 41

- Alignment No. 15376  
- gi No. 3097244  
- % Identity 71.4  
- Alignment Length 42  
- Location of Alignment in SEQ ID NO 2556: from 1 to 41

- Alignment No. 15377  
- gi No. 3122785  
- % Identity 78  
- Alignment Length 41  
- Location of Alignment in SEQ ID NO 2556: from 1 to 41

- Alignment No. 15378  
- gi No. 4574240  
- % Identity 76.2  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2556: from 21 to 41

- Alignment No. 15379  
- gi No. 4678226  
- % Identity 80.5  
- Alignment Length 41  
- Location of Alignment in SEQ ID NO 2556: from 1 to 41

- Alignment No. 15380  
- gi No. 4886269  
- % Identity 82.9  
- Alignment Length 41

- Location of Alignment in SEQ ID NO 2556: from 1 to 41

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2557
- Ceres seq\_id 1503813
- Location of start within SEQ ID NO 2554: at 295 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15381
- Ribosomal protein S11
- Location within SEQ ID NO 2557: from 3 to 68 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15382
- gi No. 1173200
- % Identity 90.2
- Alignment Length 41
- Location of Alignment in SEQ ID NO 2557: from 28 to 68
- Alignment No. 15383
- gi No. 1173201
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15384
- gi No. 131772
- % Identity 97
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15385
- gi No. 131773
- % Identity 95.5
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15386
- gi No. 133771
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15387
- gi No. 133777
- % Identity 80.3
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15388
- gi No. 133782
- % Identity 82.4
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2557: from 3 to 68
- Alignment No. 15389
- gi No. 133785
- % Identity 89.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15390  
- gi No. 133789  
- % Identity 75.8  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15391  
- gi No. 1346941  
- % Identity 77.3  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15392  
- gi No. 1350935  
- % Identity 83.3  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15393  
- gi No. 1350937  
- % Identity 84.8  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15394  
- gi No. 2350992  
- % Identity 72.1  
- Alignment Length 68  
- Location of Alignment in SEQ ID NO 2557: from 3 to 69

- Alignment No. 15395  
- gi No. 2414647  
- % Identity 77.3  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15396  
- gi No. 2500442  
- % Identity 74.4  
- Alignment Length 39  
- Location of Alignment in SEQ ID NO 2557: from 3 to 41

- Alignment No. 15397  
- gi No. 2500443  
- % Identity 87  
- Alignment Length 23  
- Location of Alignment in SEQ ID NO 2557: from 46 to 68

- Alignment No. 15398  
- gi No. 3097244  
- % Identity 89.4  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15399  
- gi No. 3122785  
- % Identity 95.5  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15400  
- gi No. 4574240  
- % Identity 84.8  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15401  
- gi No. 4588920  
- % Identity 86.4  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15402  
- gi No. 4678226  
- % Identity 93.9  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15403  
- gi No. 4886269  
- % Identity 93.9  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15404  
- gi No. 5032051  
- % Identity 89.4  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15405  
- gi No. 5441523  
- % Identity 91.7  
- Alignment Length 36  
- Location of Alignment in SEQ ID NO 2557: from 33 to 68

- Alignment No. 15406  
- gi No. 547604  
- % Identity 78.8  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15407  
- gi No. 70946  
- % Identity 77.3  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15408  
- gi No. 730453  
- % Identity 78.8  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15409  
- gi No. 730633  
- % Identity 84.8  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

- Alignment No. 15410

- gi No. 83794
- % Identity 84.8
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2557: from 3 to 68

Maximum Length Sequence corresponding to clone ID 315681

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2558
- Ceres seq\_id 1503822

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2559
- Ceres seq\_id 1503823
- Location of start within SEQ ID NO 2558: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15411
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2559: from 57 to 150 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2560
- Ceres seq\_id 1503824
- Location of start within SEQ ID NO 2558: at 84 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15412
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2560: from 30 to 123 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2561
- Ceres seq\_id 1503825
- Location of start within SEQ ID NO 2558: at 150 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15413
- 6,7-dimethyl-8-ribityllumazine synthase
- Location within SEQ ID NO 2561: from 8 to 101 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 315697

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2562
- Ceres seq\_id 1503826

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2563
- Ceres seq\_id 1503827
- Location of start within SEQ ID NO 2562: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 15414

- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2563: from 99 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2564
- Ceres seq\_id 1503828
- Location of start within SEQ ID NO 2562: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15415
- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2564: from 92 to 110

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2565
- Ceres seq\_id 1503829
- Location of start within SEQ ID NO 2562: at 61 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15416
- gi No. 1834333
- % Identity 89.5
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2565: from 79 to 97

Maximum Length Sequence corresponding to clone ID 315810

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2566
- Ceres seq\_id 1503869

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2567
- Ceres seq\_id 1503870
- Location of start within SEQ ID NO 2566: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2568
- Ceres seq\_id 1503871
- Location of start within SEQ ID NO 2566: at 219 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15417
- gi No. 2072023
- % Identity 82.3
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2568: from 3 to 81
- Alignment No. 15418



- gi No. 2245008  
- % Identity 91.2  
- Alignment Length 68  
- Location of Alignment in SEQ ID NO 2568: from 14 to 81

- Alignment No. 15419  
- gi No. 2583137  
- % Identity 88  
- Alignment Length 50  
- Location of Alignment in SEQ ID NO 2568: from 32 to 81

- Alignment No. 15420  
- gi No. 2961343  
- % Identity 87.9  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2568: from 17 to 81

- Alignment No. 15421  
- gi No. 3024687  
- % Identity 82.3  
- Alignment Length 79  
- Location of Alignment in SEQ ID NO 2568: from 3 to 81

- Alignment No. 15422  
- gi No. 3367536  
- % Identity 78.5  
- Alignment Length 93  
- Location of Alignment in SEQ ID NO 2568: from 1 to 81

- Alignment No. 15423  
- gi No. 3810848  
- % Identity 74.7  
- Alignment Length 79  
- Location of Alignment in SEQ ID NO 2568: from 3 to 81

- Alignment No. 15424  
- gi No. 4581162  
- % Identity 87.8  
- Alignment Length 82  
- Location of Alignment in SEQ ID NO 2568: from 1 to 81

- Alignment No. 15425  
- gi No. 4773906  
- % Identity 76.8  
- Alignment Length 82  
- Location of Alignment in SEQ ID NO 2568: from 1 to 81

- Alignment No. 15426  
- gi No. 4895235  
- % Identity 82.1  
- Alignment Length 78  
- Location of Alignment in SEQ ID NO 2568: from 4 to 81

- Alignment No. 15427  
- gi No. 586441  
- % Identity 72.2  
- Alignment Length 79  
- Location of Alignment in SEQ ID NO 2568: from 3 to 81

Maximum Length Sequence corresponding to clone ID 315827  
(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2569
- Ceres seq\_id 1503873
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2570
  - Ceres seq\_id 1503874
  - Location of start within SEQ ID NO 2569: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2571
  - Ceres seq\_id 1503875
  - Location of start within SEQ ID NO 2569: at 8 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2572
  - Ceres seq\_id 1503876
  - Location of start within SEQ ID NO 2569: at 58 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15428
- gi No. 4539333
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2572: from 52 to 65

Maximum Length Sequence corresponding to clone ID 315859

- (A) Polynucleotide Sequence
  - Pat. Appln. SEQ ID NO 2573
  - Ceres seq\_id 1503886
- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2574
  - Ceres seq\_id 1503887
  - Location of start within SEQ ID NO 2573: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2575
  - Ceres seq\_id 1503888
  - Location of start within SEQ ID NO 2573: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- (B) Polypeptide Sequence
  - Pat. Appln. SEQ ID NO 2576
  - Ceres seq\_id 1503889
  - Location of start within SEQ ID NO 2573: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15429
- gi No. 3387886
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2576: from 1 to 12
- Alignment No. 15430
- gi No. 3402680
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2576: from 3 to 14

Maximum Length Sequence corresponding to clone ID 315865

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2577
- Ceres seq\_id 1503890

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2578
- Ceres seq\_id 1503891
- Location of start within SEQ ID NO 2577: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15431
- Peroxidase
- Location within SEQ ID NO 2578: from 48 to 111 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15432
- gi No. 1076635
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2578: from 68 to 82
- Alignment No. 15433
- gi No. 5002334
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2578: from 74 to 111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2579
- Ceres seq\_id 1503892
- Location of start within SEQ ID NO 2577: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2580
- Ceres seq\_id 1503893
- Location of start within SEQ ID NO 2577: at 22 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15434
- Peroxidase

- Location within SEQ ID NO 2580: from 41 to 104 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15435
- gi No. 1076635
- % Identity 86.7
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2580: from 61 to 75
- Alignment No. 15436
- gi No. 5002334
- % Identity 73.7
- Alignment Length 38
- Location of Alignment in SEQ ID NO 2580: from 67 to 104

Maximum Length Sequence corresponding to clone ID 315868

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2581
- Ceres seq\_id 1503894

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2582
- Ceres seq\_id 1503895
- Location of start within SEQ ID NO 2581: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15437
- gi No. 1142653
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2582: from 79 to 157
- Alignment No. 15438
- gi No. 128844
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2582: from 53 to 76
- Alignment No. 15439
- gi No. 4539408
- % Identity 70.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 2582: from 36 to 159
- Alignment No. 15440
- gi No. 5031931
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2582: from 79 to 157
- Alignment No. 15441
- gi No. 92559
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2582: from 53 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2583
- Ceres seq\_id 1503896
- Location of start within SEQ ID NO 2581: at 68 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15442
- gi No. 1142653
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2583: from 57 to 135
  
- Alignment No. 15443
- gi No. 128844
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2583: from 31 to 54
  
- Alignment No. 15444
- gi No. 4539408
- % Identity 70.2
- Alignment Length 125
- Location of Alignment in SEQ ID NO 2583: from 14 to 137
  
- Alignment No. 15445
- gi No. 5031931
- % Identity 74.7
- Alignment Length 79
- Location of Alignment in SEQ ID NO 2583: from 57 to 135
  
- Alignment No. 15446
- gi No. 92559
- % Identity 70.8
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2583: from 31 to 54

Maximum Length Sequence corresponding to clone ID 315884

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2584
- Ceres seq\_id 1503899

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2585
- Ceres seq\_id 1503900
- Location of start within SEQ ID NO 2584: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15447
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2585: from 69 to 106 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2586
- Ceres seq\_id 1503901
- Location of start within SEQ ID NO 2584: at 18 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15448
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2586: from 64 to 101 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2587
- Ceres seq\_id 1503902
- Location of start within SEQ ID NO 2584: at 147 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15449
- Topoisomerase DNA binding C4 zinc finger
- Location within SEQ ID NO 2587: from 21 to 58 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316031

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2588
- Ceres seq\_id 1503924

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2589
- Ceres seq\_id 1503925
- Location of start within SEQ ID NO 2588: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15450
- gi No. 3004565
- % Identity 80
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2589: from 1 to 80

Maximum Length Sequence corresponding to clone ID 316062

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2590
- Ceres seq\_id 1503926

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2591
- Ceres seq\_id 1503927
- Location of start within SEQ ID NO 2590: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15451
- Protein phosphatase 2C
- Location within SEQ ID NO 2591: from 24 to 163 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15452
- gi No. 3927836
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2591: from 3 to 13

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2592
- Ceres seq\_id 1503928
- Location of start within SEQ ID NO 2590: at 17 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15453
- Protein phosphatase 2C
- Location within SEQ ID NO 2592: from 19 to 158 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2593
- Ceres seq\_id 1503929
- Location of start within SEQ ID NO 2590: at 47 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15454
- Protein phosphatase 2C
- Location within SEQ ID NO 2593: from 9 to 148 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316101

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2594
- Ceres seq\_id 1503934

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2595
- Ceres seq\_id 1503935
- Location of start within SEQ ID NO 2594: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2596
- Ceres seq\_id 1503936
- Location of start within SEQ ID NO 2594: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15455
- gi No. 3822340
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2596: from 37 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2597
- Ceres seq\_id 1503937
- Location of start within SEQ ID NO 2594: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316143

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2598
- Ceres seq\_id 1503942

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2599
- Ceres seq\_id 1503943
- Location of start within SEQ ID NO 2598: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15456
- gi No. 5441235
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2599: from 74 to 84

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2600
- Ceres seq\_id 1503944
- Location of start within SEQ ID NO 2598: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15457
- Sperm histone P2
- Location within SEQ ID NO 2600: from 38 to 118 aa.

#### (D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2601
- Ceres seq\_id 1503945
- Location of start within SEQ ID NO 2598: at 124 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- ```
- Alignment No. 15458
- gi No. 5441235
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2601: from 33 to 43
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Maximum Length Sequence corresponding to clone ID 316146

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2602
- Ceres seq id 1503946

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2603
- Ceres seq\_id 1503947
- Location of start within SEQ ID NO 2602: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15459
- Phosphoribosyl pyrophosphate synthetase
- Location within SEO ID NO 2603: from 1 to 80 aa.

#### (D) Related Amino Acid Sequences

- Alignment No. 15460
- gi No. 2833379
- % Identity 87.7
- Alignment Length 81



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Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15461
- gi No. 2833380
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15462
- gi No. 2833468
- % Identity 76.3
- Alignment Length 80
- Location of Alignment in SEQ ID NO 2603: from 1 to 80

- Alignment No. 15463
- gi No. 2842627
- % Identity 77.8
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15464
- gi No. 3128195
- % Identity 90.1
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15465
- gi No. 4902849
- % Identity 96.3
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

- Alignment No. 15466
- gi No. 4902851
- % Identity 91.4
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2603: from 1 to 81

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(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2604
- Ceres seq\_id 1503948
- Location of start within SEQ ID NO 2602: at 80 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15467
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2604: from 1 to 54 aa.

#### (D) Related Amino Acid Sequences

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- Alignment No. 15468
- gi No. 2833379
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55

- Alignment No. 15469
- gi No. 2833380
- % Identity 87.7
- Alignment Length 81
- Location of Alignment in SEQ ID NO 2604: from 1 to 55

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- Alignment No. 15470
  - gi No. 2833468
  - % Identity 76.3
  - Alignment Length 80
  - Location of Alignment in SEQ ID NO 2604: from 1 to 54
- Alignment No. 15471
  - gi No. 2842627
  - % Identity 77.8
  - Alignment Length 81
  - Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15472
  - gi No. 3128195
  - % Identity 90.1
  - Alignment Length 81
  - Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15473
  - gi No. 4902849
  - % Identity 96.3
  - Alignment Length 81
  - Location of Alignment in SEQ ID NO 2604: from 1 to 55
- Alignment No. 15474
  - gi No. 4902851
  - % Identity 91.4
  - Alignment Length 81
  - Location of Alignment in SEQ ID NO 2604: from 1 to 55

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2605
- Ceres seq\_id 1503949
- Location of start within SEQ ID NO 2602: at 280 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15475
- Phosphoribosyl pyrophosphate synthetase
- Location within SEQ ID NO 2605: from 1 to 70 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15476
- gi No. 4902849
- % Identity 71.6
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2605: from 1 to 70

Maximum Length Sequence corresponding to clone ID 316227

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2606
- Ceres seq\_id 1503969

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2607
- Ceres seq\_id 1503970
- Location of start within SEQ ID NO 2606: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15477
- gi No. 4587514
- % Identity 94.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59
- Alignment No. 15478
- gi No. 5531833
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59
- Alignment No. 15479
- gi No. 5531851
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2607: from 1 to 59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2608
- Ceres seq\_id 1503971
- Location of start within SEQ ID NO 2606: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 15480
- gi No. 4587514
- % Identity 94.9
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48
- Alignment No. 15481
- gi No. 5531833
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48
- Alignment No. 15482
- gi No. 5531851
- % Identity 71.2
- Alignment Length 59
- Location of Alignment in SEQ ID NO 2608: from 1 to 48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2609
- Ceres seq\_id 1503972
- Location of start within SEQ ID NO 2606: at 184 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316265

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2610
- Ceres seq\_id 1503989

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2611
- Ceres seq\_id 1503990
- Location of start within SEQ ID NO 2610: at 67 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15483
- EF hand
- Location within SEQ ID NO 2611: from 48 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15484
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15485
- gi No. 1076792
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15486
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15487
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15488
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15489
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2611: from 14 to 145
- Alignment No. 15490
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15491
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15492
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

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- Alignment No. 15493
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15494
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145

- Alignment No. 15495
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15496
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15497
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145

- Alignment No. 15498
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15499
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15500
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15501
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15502
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

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- Alignment No. 15503
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2611: from 75 to 104
  
- Alignment No. 15504
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15505
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15506
- gi No. 115518
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15507
- gi No. 115519
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15508
- gi No. 115520
- % Identity 87
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15509
- gi No. 115521
- % Identity 89.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15510
- gi No. 115522
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15511
- gi No. 115523
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
  
- Alignment No. 15512
- gi No. 115524
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15513

- gi No. 115525
- % Identity 97.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15514
- gi No. 115526
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15515
- gi No. 115527
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
  
- Alignment No. 15516
- gi No. 115528
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15517
- gi No. 115530
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15518
- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15519
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15520
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 12 to 142
  
- Alignment No. 15521
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15522
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15523
- gi No. 1168749

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15524
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15525
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15526
- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15527
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2611: from 77 to 145
  
- Alignment No. 15528
- gi No. 1345451
- % Identity 94.8
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2611: from 2 to 59
  
- Alignment No. 15529
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15530
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15531
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15532
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15533
- gi No. 1421816
- % Identity 85.5



- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15534  
- gi No. 1565285  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15535  
- gi No. 162030  
- % Identity 89.7  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15536  
- gi No. 16225  
- % Identity 99.3  
- Alignment Length 135  
- Location of Alignment in SEQ ID NO 2611: from 12 to 145

- Alignment No. 15537  
- gi No. 166655  
- % Identity 98.6  
- Alignment Length 140  
- Location of Alignment in SEQ ID NO 2611: from 7 to 145

- Alignment No. 15538  
- gi No. 167676  
- % Identity 87.4  
- Alignment Length 135  
- Location of Alignment in SEQ ID NO 2611: from 12 to 145

- Alignment No. 15539  
- gi No. 168777  
- % Identity 82.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15540  
- gi No. 169406  
- % Identity 88  
- Alignment Length 75  
- Location of Alignment in SEQ ID NO 2611: from 41 to 115

- Alignment No. 15541  
- gi No. 170076  
- % Identity 79.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15542  
- gi No. 1705567  
- % Identity 85.4  
- Alignment Length 144  
- Location of Alignment in SEQ ID NO 2611: from 3 to 145

- Alignment No. 15543  
- gi No. 1754997  
- % Identity 98.3  
- Alignment Length 121

- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15544
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15545
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15546
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2611: from 16 to 145
- Alignment No. 15547
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2611: from 57 to 119
- Alignment No. 15548
- gi No. 20186
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15549
- gi No. 208092
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15550
- gi No. 2119350
- % Identity 92.2
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2611: from 77 to 127
- Alignment No. 15551
- gi No. 2119353
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15552
- gi No. 2119360
- % Identity 99.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145
- Alignment No. 15553
- gi No. 2119361
- % Identity 94.2
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2611: from 26 to 145

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- Alignment No. 15554
- gi No. 2119362
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15555
- gi No. 2119364
- % Identity 90
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 94 to 113

- Alignment No. 15556
- gi No. 2129557
- % Identity 96.8
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31

- Alignment No. 15557
- gi No. 2129558
- % Identity 93.5
- Alignment Length 31
- Location of Alignment in SEQ ID NO 2611: from 1 to 31

- Alignment No. 15558
- gi No. 2129978
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15559
- gi No. 2147165
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15560
- gi No. 2181205
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15561
- gi No. 222925
- % Identity 92.6
- Alignment Length 136
- Location of Alignment in SEQ ID NO 2611: from 8 to 143

- Alignment No. 15562
- gi No. 223036
- % Identity 88.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15563
- gi No. 223218
- % Identity 89
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

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- Alignment No. 15564
- gi No. 223872
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15565
- gi No. 2244820
- % Identity 75.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15566
- gi No. 225024
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2611: from 3 to 145
- Alignment No. 15567
- gi No. 2267084
- % Identity 94.1
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2611: from 12 to 145
- Alignment No. 15568
- gi No. 228408
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2611: from 14 to 145
- Alignment No. 15569
- gi No. 2291247
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15570
- gi No. 230381
- % Identity 88.2
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2611: from 79 to 145
- Alignment No. 15571
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2611: from 81 to 145
- Alignment No. 15572
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2611: from 9 to 126
- Alignment No. 15573
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2611: from 1 to 104
- Alignment No. 15574

- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
  
- Alignment No. 15575
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 61 to 145
  
- Alignment No. 15576
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2611: from 32 to 70
  
- Alignment No. 15577
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2611: from 77 to 133
  
- Alignment No. 15578
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2611: from 108 to 127
  
- Alignment No. 15579
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2611: from 2 to 76
  
- Alignment No. 15580
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15581
- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2611: from 38 to 123
  
- Alignment No. 15582
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2611: from 96 to 129
  
- Alignment No. 15583
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2611: from 20 to 129
  
- Alignment No. 15584
- gi No. 2809481

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15585
- gi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2611: from 8 to 141
- Alignment No. 15586
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15587
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2611: from 8 to 129
- Alignment No. 15588
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2611: from 74 to 141
- Alignment No. 15589
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15590
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15591
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15592
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15593
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2611: from 77 to 111
- Alignment No. 15594
- gi No. 3336912
- % Identity 93.8

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15595
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2611: from 28 to 145
- Alignment No. 15596
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15597
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2611: from 32 to 60
- Alignment No. 15598
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 108 to 126
- Alignment No. 15599
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2611: from 128 to 145
- Alignment No. 15600
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15601
- gi No. 3561061
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15602
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15603
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15604
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15605  
- gi No. 3800849  
- % Identity 87.7  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15606  
- gi No. 3800851  
- % Identity 72.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15607  
- gi No. 3913191  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15608  
- gi No. 4028590  
- % Identity 82.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15609  
- gi No. 4033343  
- % Identity 82.1  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15610  
- gi No. 4033509  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15611  
- gi No. 4098293  
- % Identity 95.3  
- Alignment Length 107  
- Location of Alignment in SEQ ID NO 2611: from 20 to 126

- Alignment No. 15612  
- gi No. 4098295  
- % Identity 86  
- Alignment Length 107  
- Location of Alignment in SEQ ID NO 2611: from 20 to 126

- Alignment No. 15613  
- gi No. 4103778  
- % Identity 94.1  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2611: from 130 to 145

- Alignment No. 15614  
- gi No. 4103959  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145



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- Alignment No. 15615
- gi No. 4103963
- % Identity 100
- Alignment Length 65
- Location of Alignment in SEQ ID NO 2611: from 82 to 145

- Alignment No. 15616
- gi No. 4103965
- % Identity 100
- Alignment Length 64
- Location of Alignment in SEQ ID NO 2611: from 83 to 145

- Alignment No. 15617
- gi No. 4150908
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15618
- gi No. 4200039
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15619
- gi No. 4335787
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15620
- gi No. 4336136
- % Identity 87.2
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2611: from 21 to 67

- Alignment No. 15621
- gi No. 4379369
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15622
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15623
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15624
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
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- Alignment No. 15625
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
- Alignment No. 15626
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15627
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15628
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15629
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2611: from 70 to 145
- Alignment No. 15630
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 3 to 144
- Alignment No. 15631
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15632
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15633
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15634
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15635

- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15636
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15637
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15638
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15639
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15640
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15641
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15642
- gi No. 4959150
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15643
- gi No. 4959151
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15644
- gi No. 4959152
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
  
- Alignment No. 15645
- gi No. 4959153

- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15646
- gi No. 4959154
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15647
- gi No. 4959155
- % Identity 92.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15648
- gi No. 4959156
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15649
- gi No. 4959157
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15650
- gi No. 4959159
- % Identity 89
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15651
- gi No. 4959160
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15652
- gi No. 4959161
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15653
- gi No. 4959162
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15654
- gi No. 4959163
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15655
- gi No. 4959164
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15656
- gi No. 4959165
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15657
- gi No. 4959166
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15658
- gi No. 4959167
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15659
- gi No. 4959168
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15660
- gi No. 4959169
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15661
- gi No. 4959170
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15662
- gi No. 4959171
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15663
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15664
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15665
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15666
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15667
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15668
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15669
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15670
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15671
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15672
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15673
- gi No. 4959612
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15674
- gi No. 4959613
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15675
- gi No. 4959614
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15676  
- gi No. 4959615  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15677  
- gi No. 4959616  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15678  
- gi No. 4959617  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15679  
- gi No. 4959618  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15680  
- gi No. 4959621  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15681  
- gi No. 4959622  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15682  
- gi No. 4959625  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15683  
- gi No. 4959626  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15684  
- gi No. 4959629  
- % Identity 94.6  
- Alignment Length 149  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15685  
- gi No. 4959630  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15686  
- gi No. 4959635  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15687  
- gi No. 4959636  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15688  
- gi No. 4959637  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15689  
- gi No. 4959638  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15690  
- gi No. 4959640  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15691  
- gi No. 4959645  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15692  
- gi No. 4959646  
- % Identity 96.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15693  
- gi No. 4959647  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15694  
- gi No. 4959648  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15695  
- gi No. 4959673  
- % Identity 100  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2611: from 49 to 70

- Alignment No. 15696

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- gi No. 4995696  
- % Identity 95.5  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2611: from 49 to 70

- Alignment No. 15697  
- gi No. 4995737  
- % Identity 82.6  
- Alignment Length 23  
- Location of Alignment in SEQ ID NO 2611: from 49 to 71

- Alignment No. 15698  
- gi No. 4995739  
- % Identity 91.3  
- Alignment Length 23  
- Location of Alignment in SEQ ID NO 2611: from 49 to 71

- Alignment No. 15699  
- gi No. 508526  
- % Identity 90.8  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 2611: from 1 to 131

- Alignment No. 15700  
- gi No. 535428  
- % Identity 76  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15701  
- gi No. 552252  
- % Identity 84.6  
- Alignment Length 26  
- Location of Alignment in SEQ ID NO 2611: from 75 to 100

- Alignment No. 15702  
- gi No. 5640002  
- % Identity 91.3  
- Alignment Length 80  
- Location of Alignment in SEQ ID NO 2611: from 61 to 140

- Alignment No. 15703  
- gi No. 565166  
- % Identity 86.2  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15704  
- gi No. 576081  
- % Identity 89.4  
- Alignment Length 141  
- Location of Alignment in SEQ ID NO 2611: from 6 to 145

- Alignment No. 15705  
- gi No. 587454  
- % Identity 90.5  
- Alignment Length 137  
- Location of Alignment in SEQ ID NO 2611: from 10 to 145

- Alignment No. 15706  
- gi No. 625985

- % Identity 95.7  
- Alignment Length 46  
- Location of Alignment in SEQ ID NO 2611: from 1 to 46

- Alignment No. 15707  
- gi No. 640285  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15708  
- gi No. 640294  
- % Identity 90.8  
- Alignment Length 142  
- Location of Alignment in SEQ ID NO 2611: from 5 to 145

- Alignment No. 15709  
- gi No. 71660  
- % Identity 90.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15710  
- gi No. 71662  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15711  
- gi No. 71667  
- % Identity 91.7  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15712  
- gi No. 71673  
- % Identity 90.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15713  
- gi No. 71676  
- % Identity 84.8  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2611: from 2 to 145

- Alignment No. 15714  
- gi No. 729010  
- % Identity 98.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15715  
- gi No. 729011  
- % Identity 82.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2611: from 1 to 145

- Alignment No. 15716  
- gi No. 729012  
- % Identity 87.3

- Alignment Length 142
- Location of Alignment in SEQ ID NO 2611: from 5 to 145
- Alignment No. 15717
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2611: from 2 to 145
- Alignment No. 15718
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2611: from 2 to 142
- Alignment No. 15719
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2611: from 1 to 145
- Alignment No. 15720
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2611: from 3 to 74

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2612
- Ceres seq\_id 1503991
- Location Of start within SEQ ID NO 2610: at 175 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15721
- EF hand
- Location within SEQ ID NO 2612: from 12 to 40 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15722
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15723
- gi No. 1076792
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15724
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15725
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15726
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15727
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15728
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15729
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15730
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15731
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15732
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15733
- gi No. 115503
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15734
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15735
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15736
  - gi No. 115508
  - % Identity 91.8
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15737
  - gi No. 115509
  - % Identity 90.4
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15738
  - gi No. 115510
  - % Identity 90.3
  - Alignment Length 145
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15739
  - gi No. 115511
  - % Identity 100
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15740
  - gi No. 115513
  - % Identity 93.2
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15741
  - gi No. 115514
  - % Identity 80
  - Alignment Length 30
  - Location of Alignment in SEQ ID NO 2612: from 39 to 68
- Alignment No. 15742
  - gi No. 115515
  - % Identity 98.6
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15743
  - gi No. 115516
  - % Identity 91
  - Alignment Length 145
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15744
  - gi No. 115518
  - % Identity 90.3
  - Alignment Length 145
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15745
  - gi No. 115519
  - % Identity 91.8
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15746  
- gi No. 115520  
- % Identity 87  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15747  
- gi No. 115521  
- % Identity 89.7  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15748  
- gi No. 115522  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15749  
- gi No. 115523  
- % Identity 75.4  
- Alignment Length 142  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15750  
- gi No. 115524  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15751  
- gi No. 115525  
- % Identity 97.9  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15752  
- gi No. 115526  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15753  
- gi No. 115527  
- % Identity 87  
- Alignment Length 77  
- Location of Alignment in SEQ ID NO 2612: from 34 to 109

- Alignment No. 15754  
- gi No. 115528  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15755  
- gi No. 115530  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15756

- ```

- gi No. 115531
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15757
- gi No. 115532
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15758
- gi No. 115534
- % Identity 93.1
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 106

- Alignment No. 15759
- gi No. 115541
- % Identity 83.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15760
- gi No. 1168748
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15761
- gi No. 1168749
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15762
- gi No. 1235664
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15763
- gi No. 1292710
- % Identity 97.3
- Alignment Length 147
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15764
- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15765
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2612: from 41 to 109

- Alignment No. 15766
- gi No. 1345451

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- % Identity 94.8  
- Alignment Length 58  
- Location of Alignment in SEQ ID NO 2612: from 1 to 23

- Alignment No. 15767  
- gi No. 1345660  
- % Identity 98.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15768  
- gi No. 1345661  
- % Identity 87.7  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15769  
- gi No. 1362058  
- % Identity 96.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15770  
- gi No. 1402947  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15771  
- gi No. 1421816  
- % Identity 85.5  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15772  
- gi No. 1565285  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15773  
- gi No. 162030  
- % Identity 89.7  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15774  
- gi No. 16225  
- % Identity 99.3  
- Alignment Length 135  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15775  
- gi No. 166655  
- % Identity 98.6  
- Alignment Length 140  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15776  
- gi No. 167676  
- % Identity 87.4



- Alignment Length 135
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15777
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15778
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 5 to 79
- Alignment No. 15779
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15780
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15781
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15782
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15783
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
- Alignment No. 15784
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15785
- gi No. 1785958
- % Identity 87.3
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2612: from 21 to 83
- Alignment No. 15786
- gi No. 20186
- % Identity 99.3
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15787  
- gi No. 208092  
- % Identity 96.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15788  
- gi No. 2119350  
- % Identity 92.2  
- Alignment Length 51  
- Location of Alignment in SEQ ID NO 2612: from 41 to 91

- Alignment No. 15789  
- gi No. 2119353  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15790  
- gi No. 2119360  
- % Identity 99.2  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15791  
- gi No. 2119361  
- % Identity 94.2  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15792  
- gi No. 2119362  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15793  
- gi No. 2119364  
- % Identity 90  
- Alignment Length 20  
- Location of Alignment in SEQ ID NO 2612: from 58 to 77

- Alignment No. 15794  
- gi No. 2129978  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15795  
- gi No. 2147165  
- % Identity 98.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15796  
- gi No. 2181205  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15797  
- gi No. 222925  
- % Identity 92.6  
- Alignment Length 136  
- Location of Alignment in SEQ ID NO 2612: from 1 to 107

- Alignment No. 15798  
- gi No. 223036  
- % Identity 88.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15799  
- gi No. 223218  
- % Identity 89  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15800  
- gi No. 223872  
- % Identity 86.9  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15801  
- gi No. 2244820  
- % Identity 75.4  
- Alignment Length 142  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15802  
- gi No. 225024  
- % Identity 87.5  
- Alignment Length 144  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15803  
- gi No. 2267084  
- % Identity 94.1  
- Alignment Length 135  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15804  
- gi No. 228408  
- % Identity 97.7  
- Alignment Length 133  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15805  
- gi No. 2291247  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15806  
- gi No. 230381  
- % Identity 88.2  
- Alignment Length 68  
- Location of Alignment in SEQ ID NO 2612: from 43 to 109

- Alignment No. 15807
- gi No. 230382
- % Identity 86.4
- Alignment Length 66
- Location of Alignment in SEQ ID NO 2612: from 45 to 109
  
- Alignment No. 15808
- gi No. 2388889
- % Identity 99.2
- Alignment Length 118
- Location of Alignment in SEQ ID NO 2612: from 1 to 90
  
- Alignment No. 15809
- gi No. 2388891
- % Identity 95.2
- Alignment Length 104
- Location of Alignment in SEQ ID NO 2612: from 1 to 68
  
- Alignment No. 15810
- gi No. 2392137
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15811
- gi No. 2464957
- % Identity 89.5
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 25 to 109
  
- Alignment No. 15812
- gi No. 249170
- % Identity 92.3
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2612: from 1 to 34
  
- Alignment No. 15813
- gi No. 249171
- % Identity 75.4
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2612: from 41 to 97
  
- Alignment No. 15814
- gi No. 254773
- % Identity 100
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2612: from 72 to 91
  
- Alignment No. 15815
- gi No. 2554673
- % Identity 93.3
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2612: from 1 to 40
  
- Alignment No. 15816
- gi No. 2623680
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15817

- gi No. 2654179
- % Identity 93
- Alignment Length 86
- Location of Alignment in SEQ ID NO 2612: from 2 to 87
  
- Alignment No. 15818
- gi No. 266018
- % Identity 91.2
- Alignment Length 34
- Location of Alignment in SEQ ID NO 2612: from 60 to 93
  
- Alignment No. 15819
- gi No. 2677834
- % Identity 93.6
- Alignment Length 110
- Location of Alignment in SEQ ID NO 2612: from 1 to 93
  
- Alignment No. 15820
- gi No. 2809481
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15821
- gi No. 2832598
- % Identity 91.8
- Alignment Length 134
- Location of Alignment in SEQ ID NO 2612: from 1 to 105
  
- Alignment No. 15822
- gi No. 289525
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15823
- gi No. 2959326
- % Identity 71.7
- Alignment Length 130
- Location of Alignment in SEQ ID NO 2612: from 1 to 93
  
- Alignment No. 15824
- gi No. 3021331
- % Identity 83.8
- Alignment Length 68
- Location of Alignment in SEQ ID NO 2612: from 38 to 105
  
- Alignment No. 15825
- gi No. 310563
- % Identity 78.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15826
- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15827
- gi No. 3121849

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15828
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15829
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2612: from 41 to 75
  
- Alignment No. 15830
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15831
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15832
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15833
- gi No. 348265
- % Identity 100
- Alignment Length 29
- Location of Alignment in SEQ ID NO 2612: from 1 to 24
  
- Alignment No. 15834
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 72 to 90
  
- Alignment No. 15835
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2612: from 92 to 109
  
- Alignment No. 15836
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15837
- gi No. 3561061
- % Identity 95.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15838
- gi No. 3786339
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15839
- gi No. 3800845
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15840
- gi No. 3800847
- % Identity 74.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15841
- gi No. 3800849
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15842
- gi No. 3800851
- % Identity 72.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15843
- gi No. 3913191
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15844
- gi No. 4028590
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15845
- gi No. 4033343
- % Identity 82.1
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15846
- gi No. 4033509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
- Alignment No. 15847
- gi No. 4098293
- % Identity 95.3
- Alignment Length 107

- Location of Alignment in SEQ ID NO 2612: from 1 to 90

- Alignment No. 15848  
- gi No. 4098295  
- % Identity 86  
- Alignment Length 107  
- Location of Alignment in SEQ ID NO 2612: from 1 to 90

- Alignment No. 15849  
- gi No. 4103778  
- % Identity 94.1  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2612: from 94 to 109

- Alignment No. 15850  
- gi No. 4103959  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15851  
- gi No. 4103963  
- % Identity 100  
- Alignment Length 65  
- Location of Alignment in SEQ ID NO 2612: from 46 to 109

- Alignment No. 15852  
- gi No. 4103965  
- % Identity 100  
- Alignment Length 64  
- Location of Alignment in SEQ ID NO 2612: from 47 to 109

- Alignment No. 15853  
- gi No. 4150908  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15854  
- gi No. 4200039  
- % Identity 88.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15855  
- gi No. 4335787  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15856  
- gi No. 4336136  
- % Identity 87.2  
- Alignment Length 47  
- Location of Alignment in SEQ ID NO 2612: from 1 to 31

- Alignment No. 15857  
- gi No. 4379369  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109



- Alignment No. 15858  
- gi No. 443167  
- % Identity 87.6  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15859  
- gi No. 4468115  
- % Identity 91.1  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15860  
- gi No. 4502549  
- % Identity 91.1  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15861  
- gi No. 4581211  
- % Identity 87  
- Alignment Length 77  
- Location of Alignment in SEQ ID NO 2612: from 34 to 109

- Alignment No. 15862  
- gi No. 4581213  
- % Identity 78.1  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15863  
- gi No. 4585219  
- % Identity 82.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15864  
- gi No. 461684  
- % Identity 85.1  
- Alignment Length 148  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15865  
- gi No. 476851  
- % Identity 85.7  
- Alignment Length 77  
- Location of Alignment in SEQ ID NO 2612: from 34 to 109

- Alignment No. 15866  
- gi No. 484660  
- % Identity 82.4  
- Alignment Length 142  
- Location of Alignment in SEQ ID NO 2612: from 1 to 108

- Alignment No. 15867  
- gi No. 4885109  
- % Identity 89.3  
- Alignment Length 149  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15868
- gi No. 4885111
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15869
- gi No. 4930156
- % Identity 95.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15870
- gi No. 4959142
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15871
- gi No. 4959143
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15872
- gi No. 4959144
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15873
- gi No. 4959145
- % Identity 97.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15874
- gi No. 4959146
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15875
- gi No. 4959147
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15876
- gi No. 4959148
- % Identity 94
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15877
- gi No. 4959149
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15878

- gi No. 4959150  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15879  
- gi No. 4959151  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15880  
- gi No. 4959152  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15881  
- gi No. 4959153  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15882  
- gi No. 4959154  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15883  
- gi No. 4959155  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15884  
- gi No. 4959156  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15885  
- gi No. 4959157  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15886  
- gi No. 4959159  
- % Identity 89  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15887  
- gi No. 4959160  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15888  
- gi No. 4959161

- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15889  
- gi No. 4959162  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15890  
- gi No. 4959163  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15891  
- gi No. 4959164  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15892  
- gi No. 4959165  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15893  
- gi No. 4959166  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15894  
- gi No. 4959167  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15895  
- gi No. 4959168  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15896  
- gi No. 4959169  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15897  
- gi No. 4959170  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15898  
- gi No. 4959171  
- % Identity 95.9

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- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15899
- gi No. 4959172
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15900
- gi No. 4959588
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15901
- gi No. 4959590
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15902
- gi No. 4959593
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15903
- gi No. 4959594
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15904
- gi No. 4959598
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15905
- gi No. 4959599
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15906
- gi No. 4959600
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15907
- gi No. 4959602
- % Identity 94.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15908
- gi No. 4959604
- % Identity 95.9
- Alignment Length 146

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- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15909  
- gi No. 4959612  
- % Identity 93.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15910  
- gi No. 4959613  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15911  
- gi No. 4959614  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15912  
- gi No. 4959615  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15913  
- gi No. 4959616  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15914  
- gi No. 4959617  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15915  
- gi No. 4959618  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15916  
- gi No. 4959621  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15917  
- gi No. 4959622  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15918  
- gi No. 4959625  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15919  
- gi No. 4959626  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15920  
- gi No. 4959629  
- % Identity 94.6  
- Alignment Length 149  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15921  
- gi No. 4959630  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15922  
- gi No. 4959635  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15923  
- gi No. 4959636  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15924  
- gi No. 4959637  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15925  
- gi No. 4959638  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15926  
- gi No. 4959640  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15927  
- gi No. 4959645  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15928  
- gi No. 4959646  
- % Identity 96.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15929  
- gi No. 4959647  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15930  
- gi No. 4959648  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15931  
- gi No. 4995673  
- % Identity 100  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2612: from 13 to 34

- Alignment No. 15932  
- gi No. 4995696  
- % Identity 95.5  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2612: from 13 to 34

- Alignment No. 15933  
- gi No. 4995737  
- % Identity 82.6  
- Alignment Length 23  
- Location of Alignment in SEQ ID NO 2612: from 13 to 35

- Alignment No. 15934  
- gi No. 4995739  
- % Identity 91.3  
- Alignment Length 23  
- Location of Alignment in SEQ ID NO 2612: from 13 to 35

- Alignment No. 15935  
- gi No. 508526  
- % Identity 90.8  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 2612: from 1 to 95

- Alignment No. 15936  
- gi No. 535428  
- % Identity 76  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15937  
- gi No. 552252  
- % Identity 84.6  
- Alignment Length 26  
- Location of Alignment in SEQ ID NO 2612: from 39 to 64

- Alignment No. 15938  
- gi No. 5640002  
- % Identity 91.3  
- Alignment Length 80  
- Location of Alignment in SEQ ID NO 2612: from 25 to 104

- Alignment No. 15939



- gi No. 565166  
- % Identity 86.2  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15940  
- gi No. 576081  
- % Identity 89.4  
- Alignment Length 141  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15941  
- gi No. 587454  
- % Identity 90.5  
- Alignment Length 137  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15942  
- gi No. 640285  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15943  
- gi No. 640294  
- % Identity 90.8  
- Alignment Length 142  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15944  
- gi No. 71660  
- % Identity 90.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15945  
- gi No. 71662  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15946  
- gi No. 71667  
- % Identity 91.7  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15947  
- gi No. 71673  
- % Identity 90.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15948  
- gi No. 71676  
- % Identity 84.8  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2612: from 1 to 109

- Alignment No. 15949  
- gi No. 729010

- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15950
- gi No. 729011
- % Identity 82.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15951
- gi No. 729012
- % Identity 87.3
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15952
- gi No. 809298
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15953
- gi No. 85332
- % Identity 92.2
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2612: from 1 to 106
  
- Alignment No. 15954
- gi No. 9874
- % Identity 85.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2612: from 1 to 109
  
- Alignment No. 15955
- gi No. 99673
- % Identity 81.9
- Alignment Length 72
- Location of Alignment in SEQ ID NO 2612: from 1 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2613
- Ceres seq\_id 1503992
- Location of start within SEQ ID NO 2610: at 220 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 15956
- EF hand
- Location within SEQ ID NO 2613: from 1 to 25 aa.

(D) Related Amino Acid Sequences

- Alignment No. 15957
- gi No. 100665
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 15958
- gi No. 1076792
- % Identity 97.9

- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15959
- gi No. 1076793
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15960
- gi No. 1084453
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15961
- gi No. 1085679
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15962
- gi No. 115480
- % Identity 97.7
- Alignment Length 133
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15963
- gi No. 115484
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15964
- gi No. 115486
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15965
- gi No. 115489
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15966
- gi No. 115492
- % Identity 99.3
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15967
- gi No. 115500
- % Identity 91.9
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15968
- gi No. 115503
- % Identity 89.7
- Alignment Length 146

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Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15969
- gi No. 115504
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15970
- gi No. 115506
- % Identity 87.5
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15971
- gi No. 115508
- % Identity 91.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15972
- gi No. 115509
- % Identity 90.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15973
- gi No. 115510
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15974
- gi No. 115511
- % Identity 100
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15975
- gi No. 115513
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15976
- gi No. 115514
- % Identity 80
- Alignment Length 30
- Location of Alignment in SEQ ID NO 2613: from 24 to 53

- Alignment No. 15977
- gi No. 115515
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15978
- gi No. 115516
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

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- Alignment No. 15979  
- gi No. 115518  
- % Identity 90.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15980  
- gi No. 115519  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15981  
- gi No. 115520  
- % Identity 87  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15982  
- gi No. 115521  
- % Identity 89.7  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15983  
- gi No. 115522  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15984  
- gi No. 115523  
- % Identity 75.4  
- Alignment Length 142  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15985  
- gi No. 115524  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15986  
- gi No. 115525  
- % Identity 97.9  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15987  
- gi No. 115526  
- % Identity 91  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 15988  
- gi No. 115527  
- % Identity 87  
- Alignment Length 77  
- Location of Alignment in SEQ ID NO 2613: from 19 to 94

- Alignment No. 15989
  - gi No. 115528
  - % Identity 90.4
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15990
  - gi No. 115530
  - % Identity 90.4
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15991
  - gi No. 115531
  - % Identity 91.1
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15992
  - gi No. 115532
  - % Identity 97.9
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15993
  - gi No. 115534
  - % Identity 93.1
  - Alignment Length 131
  - Location of Alignment in SEQ ID NO 2613: from 1 to 91
- Alignment No. 15994
  - gi No. 115541
  - % Identity 83.6
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15995
  - gi No. 1168748
  - % Identity 95.9
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15996
  - gi No. 1168749
  - % Identity 98.6
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15997
  - gi No. 1235664
  - % Identity 85.6
  - Alignment Length 146
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15998
  - gi No. 1292710
  - % Identity 97.3
  - Alignment Length 147
  - Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 15999

- gi No. 1292853
- % Identity 88.4
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16000
- gi No. 1311052
- % Identity 88.6
- Alignment Length 70
- Location of Alignment in SEQ ID NO 2613: from 26 to 94
  
- Alignment No. 16001
- gi No. 1345660
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16002
- gi No. 1345661
- % Identity 87.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16003
- gi No. 1362058
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16004
- gi No. 1402947
- % Identity 97.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16005
- gi No. 1421816
- % Identity 85.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16006
- gi No. 1565285
- % Identity 93.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16007
- gi No. 162030
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16008
- gi No. 16225
- % Identity 99.3
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16009
- gi No. 166655

- % Identity 98.6
- Alignment Length 140
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16010
- gi No. 167676
- % Identity 87.4
- Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16011
- gi No. 168777
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16012
- gi No. 169406
- % Identity 88
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2613: from 1 to 64
- Alignment No. 16013
- gi No. 170076
- % Identity 79.5
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16014
- gi No. 1705567
- % Identity 85.4
- Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16015
- gi No. 1754997
- % Identity 98.3
- Alignment Length 121
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16016
- gi No. 1754999
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16017
- gi No. 1785953
- % Identity 84.1
- Alignment Length 63
- Location of Alignment in SEQ ID NO 2613: from 6 to 68
- Alignment No. 16018
- gi No. 1785955
- % Identity 72.5
- Alignment Length 131
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16019
- gi No. 1785958
- % Identity 87.3



- Alignment Length 63  
- Location of Alignment in SEQ ID NO 2613: from 6 to 68

- Alignment No. 16020  
- gi No. 20186  
- % Identity 99.3  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16021  
- gi No. 208092  
- % Identity 96.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16022  
- gi No. 2119350  
- % Identity 92.2  
- Alignment Length 51  
- Location of Alignment in SEQ ID NO 2613: from 26 to 76

- Alignment No. 16023  
- gi No. 2119353  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16024  
- gi No. 2119360  
- % Identity 99.2  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16025  
- gi No. 2119361  
- % Identity 94.2  
- Alignment Length 121  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16026  
- gi No. 2119362  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16027  
- gi No. 2119364  
- % Identity 90  
- Alignment Length 20  
- Location of Alignment in SEQ ID NO 2613: from 43 to 62

- Alignment No. 16028  
- gi No. 2129978  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16029  
- gi No. 2147165  
- % Identity 98.6  
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16030
  - gi No. 2181205
  - % Identity 92.5
  - Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16031
  - gi No. 222925
  - % Identity 92.6
  - Alignment Length 136
- Location of Alignment in SEQ ID NO 2613: from 1 to 92
- Alignment No. 16032
  - gi No. 223036
  - % Identity 88.3
  - Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16033
  - gi No. 223218
  - % Identity 89
  - Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16034
  - gi No. 223872
  - % Identity 86.9
  - Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16035
  - gi No. 2244820
  - % Identity 75.4
  - Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16036
  - gi No. 225024
  - % Identity 87.5
  - Alignment Length 144
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16037
  - gi No. 2267084
  - % Identity 94.1
  - Alignment Length 135
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16038
  - gi No. 228408
  - % Identity 97.7
  - Alignment Length 133
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16039
  - gi No. 2291247
  - % Identity 91.8
  - Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16040  
- gi No. 230381  
- % Identity 88.2  
- Alignment Length 68  
- Location of Alignment in SEQ ID NO 2613: from 28 to 94

- Alignment No. 16041  
- gi No. 230382  
- % Identity 86.4  
- Alignment Length 66  
- Location of Alignment in SEQ ID NO 2613: from 30 to 94

- Alignment No. 16042  
- gi No. 2388889  
- % Identity 99.2  
- Alignment Length 118  
- Location of Alignment in SEQ ID NO 2613: from 1 to 75

- Alignment No. 16043  
- gi No. 2388891  
- % Identity 95.2  
- Alignment Length 104  
- Location of Alignment in SEQ ID NO 2613: from 1 to 53

- Alignment No. 16044  
- gi No. 2392137  
- % Identity 90.3  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16045  
- gi No. 2464957  
- % Identity 89.5  
- Alignment Length 86  
- Location of Alignment in SEQ ID NO 2613: from 10 to 94

- Alignment No. 16046  
- gi No. 249170  
- % Identity 92.3  
- Alignment Length 39  
- Location of Alignment in SEQ ID NO 2613: from 1 to 19

- Alignment No. 16047  
- gi No. 249171  
- % Identity 75.4  
- Alignment Length 61  
- Location of Alignment in SEQ ID NO 2613: from 26 to 82

- Alignment No. 16048  
- gi No. 254773  
- % Identity 100  
- Alignment Length 20  
- Location of Alignment in SEQ ID NO 2613: from 57 to 76

- Alignment No. 16049  
- gi No. 2554673  
- % Identity 93.3  
- Alignment Length 75  
- Location of Alignment in SEQ ID NO 2613: from 1 to 25

- Alignment No. 16050  
- gi No. 2623680  
- % Identity 98.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16051  
- gi No. 2654179  
- % Identity 93  
- Alignment Length 86  
- Location of Alignment in SEQ ID NO 2613: from 1 to 72

- Alignment No. 16052  
- gi No. 266018  
- % Identity 91.2  
- Alignment Length 34  
- Location of Alignment in SEQ ID NO 2613: from 45 to 78

- Alignment No. 16053  
- gi No. 2677834  
- % Identity 93.6  
- Alignment Length 110  
- Location of Alignment in SEQ ID NO 2613: from 1 to 78

- Alignment No. 16054  
- gi No. 2809481  
- % Identity 98.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16055  
- gi No. 2832598  
- % Identity 91.8  
- Alignment Length 134  
- Location of Alignment in SEQ ID NO 2613: from 1 to 90

- Alignment No. 16056  
- gi No. 289525  
- % Identity 98.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16057  
- gi No. 2959326  
- % Identity 71.7  
- Alignment Length 130  
- Location of Alignment in SEQ ID NO 2613: from 1 to 78

- Alignment No. 16058  
- gi No. 3021331  
- % Identity 83.8  
- Alignment Length 68  
- Location of Alignment in SEQ ID NO 2613: from 23 to 90

- Alignment No. 16059  
- gi No. 310563  
- % Identity 78.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16060

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- gi No. 3121848
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16061
- gi No. 3121849
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16062
- gi No. 3136336
- % Identity 98.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16063
- gi No. 3243222
- % Identity 88.6
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2613: from 26 to 60

- Alignment No. 16064
- gi No. 3336912
- % Identity 93.8
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16065
- gi No. 3378652
- % Identity 100
- Alignment Length 119
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16066
- gi No. 3415119
- % Identity 89.7
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16067
- gi No. 348267
- % Identity 94.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 57 to 75

- Alignment No. 16068
- gi No. 348268
- % Identity 78.9
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2613: from 77 to 94

- Alignment No. 16069
- gi No. 3561059
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16070
- gi No. 3561061

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- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16071  
- gi No. 3786339  
- % Identity 91.1  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16072  
- gi No. 3800845  
- % Identity 82.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16073  
- gi No. 3800847  
- % Identity 74.7  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16074  
- gi No. 3800849  
- % Identity 87.7  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16075  
- gi No. 3800851  
- % Identity 72.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16076  
- gi No. 3913191  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16077  
- gi No. 4028590  
- % Identity 82.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16078  
- gi No. 4033343  
- % Identity 82.1  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16079  
- gi No. 4033509  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16080  
- gi No. 4098293  
- % Identity 95.3

- Alignment Length 107  
- Location of Alignment in SEQ ID NO 2613: from 1 to 75

- Alignment No. 16081  
- gi No. 4098295  
- % Identity 86  
- Alignment Length 107  
- Location of Alignment in SEQ ID NO 2613: from 1 to 75

- Alignment No. 16082  
- gi No. 4103778  
- % Identity 94.1  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2613: from 79 to 94

- Alignment No. 16083  
- gi No. 4103959  
- % Identity 97.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16084  
- gi No. 4103963  
- % Identity 100  
- Alignment Length 65  
- Location of Alignment in SEQ ID NO 2613: from 31 to 94

- Alignment No. 16085  
- gi No. 4103965  
- % Identity 100  
- Alignment Length 64  
- Location of Alignment in SEQ ID NO 2613: from 32 to 94

- Alignment No. 16086  
- gi No. 4150908  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16087  
- gi No. 4200039  
- % Identity 88.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16088  
- gi No. 4335787  
- % Identity 90.4  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16089  
- gi No. 4336136  
- % Identity 87.2  
- Alignment Length 47  
- Location of Alignment in SEQ ID NO 2613: from 1 to 16

- Alignment No. 16090  
- gi No. 4379369  
- % Identity 93.2  
- Alignment Length 146

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Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16091
- gi No. 443167
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16092
- gi No. 4468115
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16093
- gi No. 4502549
- % Identity 91.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16094
- gi No. 4581211
- % Identity 87
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16095
- gi No. 4581213
- % Identity 78.1
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16096
- gi No. 4585219
- % Identity 82.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16097
- gi No. 461684
- % Identity 85.1
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16098
- gi No. 476851
- % Identity 85.7
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2613: from 19 to 94
- Alignment No. 16099
- gi No. 484660
- % Identity 82.4
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 93
- Alignment No. 16100
- gi No. 4885109
- % Identity 89.3
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

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- Alignment No. 16101  
- gi No. 4885111  
- % Identity 82.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16102  
- gi No. 4930156  
- % Identity 95.9  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16103  
- gi No. 4959142  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16104  
- gi No. 4959143  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16105  
- gi No. 4959144  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16106  
- gi No. 4959145  
- % Identity 97.3  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16107  
- gi No. 4959146  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16108  
- gi No. 4959147  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16109  
- gi No. 4959148  
- % Identity 94  
- Alignment Length 149  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16110  
- gi No. 4959149  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16111  
- gi No. 4959150  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16112  
- gi No. 4959151  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16113  
- gi No. 4959152  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16114  
- gi No. 4959153  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16115  
- gi No. 4959154  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16116  
- gi No. 4959155  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16117  
- gi No. 4959156  
- % Identity 93.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16118  
- gi No. 4959157  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16119  
- gi No. 4959159  
- % Identity 89  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16120  
- gi No. 4959160  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16121

- gi No. 4959161  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16122  
- gi No. 4959162  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16123  
- gi No. 4959163  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16124  
- gi No. 4959164  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16125  
- gi No. 4959165  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16126  
- gi No. 4959166  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16127  
- gi No. 4959167  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16128  
- gi No. 4959168  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16129  
- gi No. 4959169  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16130  
- gi No. 4959170  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16131  
- gi No. 4959171

- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16132  
- gi No. 4959172  
- % Identity 96.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16133  
- gi No. 4959588  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16134  
- gi No. 4959590  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16135  
- gi No. 4959593  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16136  
- gi No. 4959594  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16137  
- gi No. 4959598  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16138  
- gi No. 4959599  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16139  
- gi No. 4959600  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16140  
- gi No. 4959602  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16141  
- gi No. 4959604  
- % Identity 95.9

- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16142  
- gi No. 4959612  
- % Identity 93.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16143  
- gi No. 4959613  
- % Identity 91.8  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16144  
- gi No. 4959614  
- % Identity 95.2  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16145  
- gi No. 4959615  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16146  
- gi No. 4959616  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16147  
- gi No. 4959617  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16148  
- gi No. 4959618  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16149  
- gi No. 4959621  
- % Identity 94.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16150  
- gi No. 4959622  
- % Identity 92.5  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16151  
- gi No. 4959625  
- % Identity 95.9  
- Alignment Length 146

- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16152
- gi No. 4959626
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16153
- gi No. 4959629
- % Identity 94.6
- Alignment Length 149
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16154
- gi No. 4959630
- % Identity 95.2
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16155
- gi No. 4959635
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16156
- gi No. 4959636
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16157
- gi No. 4959637
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16158
- gi No. 4959638
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16159
- gi No. 4959640
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16160
- gi No. 4959645
- % Identity 95.9
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
- Alignment No. 16161
- gi No. 4959646
- % Identity 96.6
- Alignment Length 146
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16162  
- gi No. 4959647  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16163  
- gi No. 4959648  
- % Identity 95.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16164  
- gi No. 4995673  
- % Identity 100  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2613: from 1 to 19

- Alignment No. 16165  
- gi No. 4995696  
- % Identity 95.5  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2613: from 1 to 19

- Alignment No. 16166  
- gi No. 4995737  
- % Identity 82.6  
- Alignment Length 23  
- Location of Alignment in SEQ ID NO 2613: from 1 to 20

- Alignment No. 16167  
- gi No. 4995739  
- % Identity 91.3  
- Alignment Length 23  
- Location of Alignment in SEQ ID NO 2613: from 1 to 20

- Alignment No. 16168  
- gi No. 508526  
- % Identity 90.8  
- Alignment Length 131  
- Location of Alignment in SEQ ID NO 2613: from 1 to 80

- Alignment No. 16169  
- gi No. 535428  
- % Identity 76  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16170  
- gi No. 552252  
- % Identity 84.6  
- Alignment Length 26  
- Location of Alignment in SEQ ID NO 2613: from 24 to 49

- Alignment No. 16171  
- gi No. 5640002  
- % Identity 91.3  
- Alignment Length 80  
- Location of Alignment in SEQ ID NO 2613: from 10 to 89

- Alignment No. 16172
- gi No. 565166
- % Identity 86.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16173
- gi No. 576081
- % Identity 89.4
- Alignment Length 141
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16174
- gi No. 587454
- % Identity 90.5
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16175
- gi No. 640285
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16176
- gi No. 640294
- % Identity 90.8
- Alignment Length 142
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16177
- gi No. 71660
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16178
- gi No. 71662
- % Identity 91
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16179
- gi No. 71667
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16180
- gi No. 71673
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16181
- gi No. 71676
- % Identity 84.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2613: from 1 to 94
  
- Alignment No. 16182



- gi No. 729010  
- % Identity 98.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16183  
- gi No. 729011  
- % Identity 82.9  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16184  
- gi No. 729012  
- % Identity 87.3  
- Alignment Length 142  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16185  
- gi No. 809298  
- % Identity 86.9  
- Alignment Length 145  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16186  
- gi No. 85332  
- % Identity 92.2  
- Alignment Length 141  
- Location of Alignment in SEQ ID NO 2613: from 1 to 91

- Alignment No. 16187  
- gi No. 9874  
- % Identity 85.6  
- Alignment Length 146  
- Location of Alignment in SEQ ID NO 2613: from 1 to 94

- Alignment No. 16188  
- gi No. 99673  
- % Identity 81.9  
- Alignment Length 72  
- Location of Alignment in SEQ ID NO 2613: from 1 to 23

Maximum Length Sequence corresponding to clone ID 316301

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2614
- Ceres seq\_id 1504001

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2615
- Ceres seq\_id 1504002
- Location of start within SEQ ID NO 2614: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2616
- Ceres seq\_id 1504003
- Location of start within SEQ ID NO 2614: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16189
- Ribosomal protein L5
- Location within SEQ ID NO 2616: from 34 to 79 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16190
- gi No. 1125808
- % Identity 80.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16191
- gi No. 1172816
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16192
- gi No. 1172817
- % Identity 90.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2616: from 27 to 79
- Alignment No. 16193
- gi No. 1172952
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2616: from 35 to 79
- Alignment No. 16194
- gi No. 1172954
- % Identity 70.6
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 26 to 76
- Alignment No. 16195
- gi No. 1172969
- % Identity 90.7
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16196
- gi No. 1173055
- % Identity 94.4
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16197
- gi No. 132649
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
- Alignment No. 16198
- gi No. 132951
- % Identity 79.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79
- Alignment No. 16199
- gi No. 132992

- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2616: from 36 to 79
  
- Alignment No. 16200
- gi No. 1350658
- % Identity 70.9
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
  
- Alignment No. 16201
- gi No. 1350659
- % Identity 70.6
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 26 to 76
  
- Alignment No. 16202
- gi No. 1710494
- % Identity 78
- Alignment Length 50
- Location of Alignment in SEQ ID NO 2616: from 30 to 79
  
- Alignment No. 16203
- gi No. 2500240
- % Identity 80.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
  
- Alignment No. 16204
- gi No. 2500241
- % Identity 78.4
- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
  
- Alignment No. 16205
- gi No. 2570507
- % Identity 85.2
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 26 to 79
  
- Alignment No. 16206
- gi No. 4322
- % Identity 77.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79
  
- Alignment No. 16207
- gi No. 4432750
- % Identity 86.1
- Alignment Length 36
- Location of Alignment in SEQ ID NO 2616: from 41 to 76
  
- Alignment No. 16208
- gi No. 4512679
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2616: from 36 to 79
  
- Alignment No. 16209
- gi No. 4586222
- % Identity 76.5

- Alignment Length 51
- Location of Alignment in SEQ ID NO 2616: from 29 to 79
- Alignment No. 16210
- gi No. 71107
- % Identity 79.6
- Alignment Length 49
- Location of Alignment in SEQ ID NO 2616: from 31 to 79

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2617
- Ceres seq\_id 1504004
- Location of start within SEQ ID NO 2614: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316327

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2618
- Ceres seq\_id 1504016

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2619
- Ceres seq\_id 1504017
- Location of start within SEQ ID NO 2618: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2620
- Ceres seq\_id 1504018
- Location of start within SEQ ID NO 2618: at 310 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16211
- gi No. 2224915
- % Identity 81.8
- Alignment Length 77
- Location of Alignment in SEQ ID NO 2620: from 1 to 55
- Alignment No. 16212
- gi No. 729944
- % Identity 75
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2620: from 1 to 55

Maximum Length Sequence corresponding to clone ID 316354

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2621
- Ceres seq\_id 1504025

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2622
- Ceres seq\_id 1504026
- Location of start within SEQ ID NO 2621: at 133 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16213
- Sugar (and other) transporter
- Location within SEQ ID NO 2622: from 1 to 98 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16214
- gi No. 2760325
- % Identity 73.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2622: from 1 to 98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2623
- Ceres seq\_id 1504027
- Location of start within SEQ ID NO 2621: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16215
- Sugar (and other) transporter
- Location within SEQ ID NO 2623: from 1 to 87 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16216
- gi No. 2760325
- % Identity 73.1
- Alignment Length 108
- Location of Alignment in SEQ ID NO 2623: from 1 to 87

Maximum Length Sequence corresponding to clone ID 316377

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2624
- Ceres seq\_id 1504036

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2625
- Ceres seq\_id 1504037
- Location of start within SEQ ID NO 2624: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16217
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2625: from 1 to 152
- Alignment No. 16218
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2625: from 1 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2626
- Ceres seq\_id 1504038
- Location of start within SEQ ID NO 2624: at 75 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16219
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2626: from 1 to 128
  
- Alignment No. 16220
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2626: from 1 to 114

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2627
- Ceres seq\_id 1504039
- Location of start within SEQ ID NO 2624: at 81 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16221
- gi No. 2505870
- % Identity 78.3
- Alignment Length 152
- Location of Alignment in SEQ ID NO 2627: from 1 to 126
  
- Alignment No. 16222
- gi No. 3287679
- % Identity 80.4
- Alignment Length 138
- Location of Alignment in SEQ ID NO 2627: from 1 to 112

Maximum Length Sequence corresponding to clone ID 316388

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2628
- Ceres seq\_id 1504044

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2629
- Ceres seq\_id 1504045
- Location of start within SEQ ID NO 2628: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16223
- gi No. 3057044
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
  
- Alignment No. 16224
- gi No. 3337356
- % Identity 93.9
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
  
- Alignment No. 16225
- gi No. 3834321

- % Identity 92.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
- Alignment No. 16226
- gi No. 3881191
- % Identity 70.5
- Alignment Length 78
- Location of Alignment in SEQ ID NO 2629: from 65 to 142
- Alignment No. 16227
- gi No. 4689112
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
- Alignment No. 16228
- gi No. 585957
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142
- Alignment No. 16229
- gi No. 585959
- % Identity 70.7
- Alignment Length 82
- Location of Alignment in SEQ ID NO 2629: from 61 to 142

Maximum Length Sequence corresponding to clone ID 316451

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2630
- Ceres seq\_id 1504050

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2631
- Ceres seq\_id 1504051
- Location of start within SEQ ID NO 2630: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16230
- WD domain, G-beta repeat
- Location within SEQ ID NO 2631: from 85 to 124 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16231
- gi No. 3122386
- % Identity 83.2
- Alignment Length 167
- Location of Alignment in SEQ ID NO 2631: from 1 to 166
- Alignment No. 16232
- gi No. 3122387
- % Identity 86.8
- Alignment Length 167
- Location of Alignment in SEQ ID NO 2631: from 1 to 166

Maximum Length Sequence corresponding to clone ID 316638

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2632
- Ceres seq\_id 1504098

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2633
- Ceres seq\_id 1504099
- Location of start within SEQ ID NO 2632: at 125 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16233
- ADP-ribosylation factor family
- Location within SEQ ID NO 2633: from 2 to 75 aa.
- Alignment No. 16234
- Ras family
- Location within SEQ ID NO 2633: from 19 to 80 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16235
- gi No. 114122
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2633: from 1 to 75
- Alignment No. 16236
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2633: from 18 to 75
- Alignment No. 16237
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2633: from 19 to 75
- Alignment No. 16238
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2633: from 19 to 75
- Alignment No. 16239
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2633: from 1 to 75
- Alignment No. 16240
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2633: from 22 to 42

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2634
- Ceres seq\_id 1504100
- Location of start within SEQ ID NO 2632: at 176 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16241
- ADP-ribosylation factor family
- Location within SEQ ID NO 2634: from 1 to 58 aa.



- Alignment No. 16242
- Ras family
- Location within SEQ ID NO 2634: from 2 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16243
- gi No. 114122
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2634: from 1 to 58

- Alignment No. 16244
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2634: from 1 to 58

- Alignment No. 16245
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2634: from 2 to 58

- Alignment No. 16246
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2634: from 2 to 58

- Alignment No. 16247
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2634: from 1 to 58

- Alignment No. 16248
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2634: from 5 to 25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2635
- Ceres seq\_id 1504101
- Location of start within SEQ ID NO 2632: at 188 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16249
- ADP-ribosylation factor family
- Location within SEQ ID NO 2635: from 1 to 54 aa.

- Alignment No. 16250
- Ras family
- Location within SEQ ID NO 2635: from 1 to 59 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16251
- gi No. 114122
- % Identity 70.7

- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16252
- gi No. 3252999
- % Identity 74.1
- Alignment Length 58
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16253
- gi No. 3746799
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16254
- gi No. 3746801
- % Identity 71.9
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16255
- gi No. 461532
- % Identity 70.7
- Alignment Length 75
- Location of Alignment in SEQ ID NO 2635: from 1 to 54
- Alignment No. 16256
- gi No. 89370
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2635: from 1 to 21

Maximum Length Sequence corresponding to clone ID 316643

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2636
- Ceres seq\_id 1504102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2637
- Ceres seq\_id 1504103
- Location of start within SEQ ID NO 2636: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16257
- gi No. 462338
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2637: from 95 to 108

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2638
- Ceres seq\_id 1504104
- Location of start within SEQ ID NO 2636: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2639
- Ceres seq\_id 1504105
- Location of start within SEQ ID NO 2636: at 94 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16258
- Merozoite Surface Antigen 2 (MSA-2) family
- Location within SEQ ID NO 2639: from 20 to 98 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316664

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2640
- Ceres seq\_id 1504107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2641
- Ceres seq\_id 1504108
- Location of start within SEQ ID NO 2640: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16259
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2641: from 65 to 155 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16260
- gi No. 1172977
- % Identity 78.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2641: from 55 to 155
- Alignment No. 16261
- gi No. 2529670
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2641: from 56 to 155
- Alignment No. 16262
- gi No. 3021348
- % Identity 75.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2641: from 58 to 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2642
- Ceres seq\_id 1504109
- Location of start within SEQ ID NO 2640: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2643
- Ceres seq\_id 1504110
- Location of start within SEQ ID NO 2640: at 164 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16263
- Eukaryotic ribosomal protein L18
- Location within SEQ ID NO 2643: from 11 to 101 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16264
- gi No. 1172977
- % Identity 78.4
- Alignment Length 102
- Location of Alignment in SEQ ID NO 2643: from 1 to 101
- Alignment No. 16265
- gi No. 2529670
- % Identity 74.3
- Alignment Length 101
- Location of Alignment in SEQ ID NO 2643: from 2 to 101
- Alignment No. 16266
- gi No. 3021348
- % Identity 75.8
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2643: from 4 to 101

Maximum Length Sequence corresponding to clone ID 316675

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2644
- Ceres seq\_id 1504111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2645
- Ceres seq\_id 1504112
- Location of start within SEQ ID NO 2644: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16267
- gi No. 121928
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2645: from 30 to 40
- Alignment No. 16268
- gi No. 121950
- % Identity 92.3
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2645: from 17 to 42

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2646
- Ceres seq\_id 1504113
- Location of start within SEQ ID NO 2644: at 49 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16269
- gi No. 121928
- % Identity 75
- Alignment Length 12

- Location of Alignment in SEQ ID NO 2646: from 14 to 24
- Alignment No. 16270
- gi No. 121950
- % Identity 92.3
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2646: from 1 to 26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2647
- Ceres seq\_id 1504114
- Location of start within SEQ ID NO 2644: at 212 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16271
- linker histone H1 and H5 family
- Location within SEQ ID NO 2647: from 1 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16272
- gi No. 121906
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2647: from 1 to 22
- Alignment No. 16273
- gi No. 121950
- % Identity 87.6
- Alignment Length 97
- Location of Alignment in SEQ ID NO 2647: from 1 to 73
- Alignment No. 16274
- gi No. 121958
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16275
- gi No. 5230781
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16276
- gi No. 5230783
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16277
- gi No. 5230785
- % Identity 76.3
- Alignment Length 93
- Location of Alignment in SEQ ID NO 2647: from 1 to 69
- Alignment No. 16278
- gi No. 5230788
- % Identity 71.6
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69

- Alignment No. 16279
- gi No. 5230790
- % Identity 70.5
- Alignment Length 95
- Location of Alignment in SEQ ID NO 2647: from 1 to 69

Maximum Length Sequence corresponding to clone ID 316686

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2648
- Ceres seq\_id 1504119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2649
- Ceres seq\_id 1504120
- Location of start within SEQ ID NO 2648: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16280
- gi No. 1085819
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2649: from 74 to 84

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2650
- Ceres seq\_id 1504121
- Location of start within SEQ ID NO 2648: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16281
- gi No. 137715
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2650: from 24 to 37
- Alignment No. 16282
- gi No. 1389772
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16283
- gi No. 1914851
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 57 to 70
- Alignment No. 16284
- gi No. 2388805
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69
- Alignment No. 16285
- gi No. 3183204
- % Identity 76.9
- Alignment Length 13

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Location of Alignment in SEQ ID NO 2650: from 57 to 69

- Alignment No. 16286
- gi No. 322755
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 25 to 38

- Alignment No. 16287
- gi No. 333063
- % Identity 71.4
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2650: from 24 to 37

- Alignment No. 16288
- gi No. 465445
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

- Alignment No. 16289
- gi No. 539029
- % Identity 71.4
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2650: from 25 to 38

- Alignment No. 16290
- gi No. 553165
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2650: from 58 to 69

- Alignment No. 16291
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

- Alignment No. 16292
- gi No. 624076
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2650: from 59 to 69

- Alignment No. 16293
- gi No. 729462
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

- Alignment No. 16294
- gi No. 93144
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2650: from 57 to 69

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(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2651
- Ceres seq\_id 1504122
- Location of start within SEQ ID NO 2648: at 90 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16295
- gi No. 1389772
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16296
- gi No. 1914851
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2651: from 28 to 41
  
- Alignment No. 16297
- gi No. 2388805
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16298
- gi No. 3183204
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16299
- gi No. 465445
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16300
- gi No. 553165
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2651: from 29 to 40
  
- Alignment No. 16301
- gi No. 553165
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16302
- gi No. 624076
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2651: from 30 to 40
  
- Alignment No. 16303
- gi No. 729462
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2651: from 28 to 40
  
- Alignment No. 16304
- gi No. 93144
- % Identity 76.9
- Alignment Length 13



- Location of Alignment in SEQ ID NO 2651: from 28 to 40

Maximum Length Sequence corresponding to clone ID 316862

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2652
- Ceres seq\_id 1504161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2653
- Ceres seq\_id 1504162
- Location of start within SEQ ID NO 2652: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16305
- gi No. 1916974
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2653: from 7 to 21
- Alignment No. 16306
- gi No. 477833
- % Identity 75
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2653: from 7 to 21

Maximum Length Sequence corresponding to clone ID 316893

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2654
- Ceres seq\_id 1504170

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2655
- Ceres seq\_id 1504171
- Location of start within SEQ ID NO 2654: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16307
- gi No. 404077
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2655: from 30 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2656
- Ceres seq\_id 1504172
- Location of start within SEQ ID NO 2654: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16308
- gi No. 4972116
- % Identity 81.8
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2656: from 26 to 36

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2657
- Ceres seq\_id 1504173

- Location of start within SEQ ID NO 2654: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16309
- gi No. 4996642
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2657: from 17 to 27

Maximum Length Sequence corresponding to clone ID 316929

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2658
- Ceres seq\_id 1504178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2659
- Ceres seq\_id 1504179
- Location of start within SEQ ID NO 2658: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16310
- GDP dissociation inhibitor
- Location within SEQ ID NO 2659: from 1 to 60 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16311
- gi No. 1550740
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16312
- gi No. 1655424
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16313
- gi No. 2384758
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16314
- gi No. 2384760
- % Identity 85.2
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16315
- gi No. 2446981
- % Identity 73.8
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16316
- gi No. 2501850
- % Identity 90.2
- Alignment Length 61

- Location of Alignment in SEQ ID NO 2659: from 1 to 60
- Alignment No. 16317
- gi No. 3175990
- % Identity 88.5
- Alignment Length 61
- Location of Alignment in SEQ ID NO 2659: from 1 to 60

Maximum Length Sequence corresponding to clone ID 316935

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2660
- Ceres seq\_id 1504180

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2661
- Ceres seq\_id 1504181
- Location of start within SEQ ID NO 2660: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2662
- Ceres seq\_id 1504182
- Location of start within SEQ ID NO 2660: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 16318
- Globin
- Location within SEQ ID NO 2662: from 44 to 168 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2663
- Ceres seq\_id 1504183
- Location of start within SEQ ID NO 2660: at 101 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 16319
- Globin
- Location within SEQ ID NO 2663: from 11 to 135 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 316946

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2664
- Ceres seq\_id 1504184

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2665
- Ceres seq\_id 1504185
- Location of start within SEQ ID NO 2664: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted

Polypeptide(s)

- Alignment No. 16320
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2665: from 1 to 134 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16321
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2665: from 3 to 139
  
- Alignment No. 16322
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2665: from 1 to 154
  
- Alignment No. 16323
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2665: from 1 to 145
  
- Alignment No. 16324
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2665: from 1 to 145
  
- Alignment No. 16325
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2665: from 3 to 139

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2666
- Ceres seq\_id 1504186
- Location of start within SEQ ID NO 2664: at 6 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16326
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2666: from 1 to 133 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16327
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2666: from 2 to 138
  
- Alignment No. 16328
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2666: from 1 to 153
  
- Alignment No. 16329
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2666: from 1 to 144

- Alignment No. 16330
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2666: from 1 to 144
- Alignment No. 16331
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2666: from 2 to 138

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2667
- Ceres seq\_id 1504187
- Location of start within SEQ ID NO 2664: at 153 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16332
- Eukaryotic protein kinase domain
- Location within SEQ ID NO 2667: from 1 to 84 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16333
- gi No. 1169128
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2667: from 1 to 89
- Alignment No. 16334
- gi No. 2253010
- % Identity 74
- Alignment Length 154
- Location of Alignment in SEQ ID NO 2667: from 1 to 104
- Alignment No. 16335
- gi No. 3063459
- % Identity 86.9
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2667: from 1 to 95
- Alignment No. 16336
- gi No. 3201541
- % Identity 87.6
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2667: from 1 to 95
- Alignment No. 16337
- gi No. 322577
- % Identity 70.8
- Alignment Length 137
- Location of Alignment in SEQ ID NO 2667: from 1 to 89

Maximum Length Sequence corresponding to clone ID 316976

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2668
- Ceres seq\_id 1504192

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2669

- Ceres seq\_id 1504193
- Location of start within SEQ ID NO 2668: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 16338
  - gi No. 5042432
  - % Identity 70.6
  - Alignment Length 68
  - Location of Alignment in SEQ ID NO 2669: from 93 to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2670
- Ceres seq\_id 1504194
- Location of start within SEQ ID NO 2668: at 87 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 16339
  - gi No. 5042432
  - % Identity 70.6
  - Alignment Length 68
  - Location of Alignment in SEQ ID NO 2670: from 65 to 131

Maximum Length Sequence corresponding to clone ID 317012

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2671
- Ceres seq\_id 1504201

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2672
- Ceres seq\_id 1504202
- Location of start within SEQ ID NO 2671: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2673
- Ceres seq\_id 1504203
- Location of start within SEQ ID NO 2671: at 369 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16340
- gi No. 2642447
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2673: from 23 to 46
  
- Alignment No. 16341
- gi No. 4335730
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2673: from 22 to 46
  
- Alignment No. 16342
- gi No. 4544385

- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2673: from 23 to 46

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2674
- Ceres seq\_id 1504204
- Location of start within SEQ ID NO 2671: at 378 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16343
- gi No. 2642447
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2674: from 20 to 43
  
- Alignment No. 16344
- gi No. 4335730
- % Identity 76.9
- Alignment Length 26
- Location of Alignment in SEQ ID NO 2674: from 19 to 43
  
- Alignment No. 16345
- gi No. 4544385
- % Identity 76
- Alignment Length 25
- Location of Alignment in SEQ ID NO 2674: from 20 to 43

Maximum Length Sequence corresponding to clone ID 317151

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2675
- Ceres seq\_id 1504231

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2676
- Ceres seq\_id 1504232
- Location of start within SEQ ID NO 2675: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16346
- gi No. 1076389
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16347
- gi No. 1076390
- % Identity 95.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16348
- gi No. 1076396
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2676: from 1 to 144
  
- Alignment No. 16349

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(B) Polypeptide Sequence  
- Pat. Appln. SEQ ID NO 2677



- Ceres seq\_id 1504233
- Location of start within SEQ ID NO 2675: at 44 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16359
- gi No. 1076389
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16360
- gi No. 1076390
- % Identity 95.2
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16361
- gi No. 1076396
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16362
- gi No. 1262171
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16363
- gi No. 1568511
- % Identity 94.5
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16364
- gi No. 2129734
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16365
- gi No. 2146743
- % Identity 92.4
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16366
- gi No. 261767
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2677: from 111 to 130
  
- Alignment No. 16367
- gi No. 3928142
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
  
- Alignment No. 16368

- gi No. 476923
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2677: from 111 to 130
- Alignment No. 16369
- gi No. 543715
- % Identity 90.3
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16370
- gi No. 5679684
- % Identity 93.8
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130
- Alignment No. 16371
- gi No. 683506
- % Identity 91.7
- Alignment Length 145
- Location of Alignment in SEQ ID NO 2677: from 1 to 130

Maximum Length Sequence corresponding to clone ID 317164

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2678
- Ceres seq\_id 1504239

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2679
- Ceres seq\_id 1504240
- Location of start within SEQ ID NO 2678: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16372
- PCI domain
- Location within SEQ ID NO 2679: from 7 to 86 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317195

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2680
- Ceres seq\_id 1504254

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2681
- Ceres seq\_id 1504255
- Location of start within SEQ ID NO 2680: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16373
- gi No. 1076294
- % Identity 81.3
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2681: from 92 to 107
- Alignment No. 16374
- gi No. 1279640
- % Identity 71.1

- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16375
- gi No. 1321924
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16376
- gi No. 1944132
- % Identity 71.1
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2681: from 64 to 107
- Alignment No. 16377
- gi No. 4972066
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2681: from 89 to 107
- Alignment No. 16378
- gi No. 5679845
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2681: from 89 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2682
- Ceres seq\_id 1504256
- Location of start within SEQ ID NO 2680: at 91 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16379
- gi No. 1279640
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16380
- gi No. 1321924
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16381
- gi No. 1944132
- % Identity 90.9
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16382
- gi No. 2894607
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32
- Alignment No. 16383
- gi No. 4585977

- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2682: from 9 to 32
- Alignment No. 16384
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
- Alignment No. 16385
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
- Alignment No. 16386
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2682: from 13 to 32
- Alignment No. 16387
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2682: from 11 to 32

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2683
- Ceres seq\_id 1504257
- Location of start within SEQ ID NO 2680: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16388
- gi No. 1279640
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
- Alignment No. 16389
- gi No. 1321924
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
- Alignment No. 16390
- gi No. 1944132
- % Identity 90.9
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
- Alignment No. 16391
- gi No. 2894607
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24
- Alignment No. 16392

- gi No. 4585977
- % Identity 75
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2683: from 1 to 24
  
- Alignment No. 16393
- gi No. 5091624
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
  
- Alignment No. 16394
- gi No. 5091626
- % Identity 75
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
  
- Alignment No. 16395
- gi No. 5306267
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2683: from 5 to 24
  
- Alignment No. 16396
- gi No. 5679845
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2683: from 3 to 24

Maximum Length Sequence corresponding to clone ID 317200

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2684
- Ceres seq\_id 1504258

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2685
- Ceres seq\_id 1504259
- Location of start within SEQ ID NO 2684: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2686
- Ceres seq\_id 1504260
- Location of start within SEQ ID NO 2684: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2687
- Ceres seq\_id 1504261
- Location of start within SEQ ID NO 2684: at 195 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16397
- gi No. 2642154

- % Identity 74.3
- Alignment Length 35
- Location of Alignment in SEQ ID NO 2687: from 1 to 35

Maximum Length Sequence corresponding to clone ID 317211

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2688
- Ceres seq\_id 1504270

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2689
- Ceres seq\_id 1504271
- Location of start within SEQ ID NO 2688: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2690
- Ceres seq\_id 1504272
- Location of start within SEQ ID NO 2688: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16398
- gi No. 1546779
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32
- Alignment No. 16399
- gi No. 2136108
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32
- Alignment No. 16400
- gi No. 3858885
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2690: from 21 to 32

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2691
- Ceres seq\_id 1504273
- Location of start within SEQ ID NO 2688: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317217

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2692
- Ceres seq\_id 1504274

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2693
- Ceres seq\_id 1504275
- Location of start within SEQ ID NO 2692: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

- Alignment No. 16401
- Metallothionein
- Location within SEQ ID NO 2693: from 37 to 88 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16402
- gi No. 1944205
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2693: from 37 to 73
- Alignment No. 16403
- gi No. 225131
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2693: from 40 to 59
- Alignment No. 16404
- gi No. 225144
- % Identity 71.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2693: from 39 to 59
- Alignment No. 16405
- gi No. 225146
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2693: from 40 to 59
- Alignment No. 16406
- gi No. 2407285
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2693: from 37 to 73
- Alignment No. 16407
- gi No. 2497897
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2693: from 37 to 84
- Alignment No. 16408
- gi No. 2497903
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2693: from 37 to 88
- Alignment No. 16409
- gi No. 2662415
- % Identity 72.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2693: from 38 to 88
- Alignment No. 16410
- gi No. 2815246
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2693: from 37 to 83

- Alignment No. 16411
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2693: from 37 to 84

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2694
- Ceres seq\_id 1504276
- Location of start within SEQ ID NO 2692: at 110 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16412
- Metallothionein
- Location within SEQ ID NO 2694: from 1 to 52 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16413
- gi No. 1944205
- % Identity 73
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2694: from 1 to 37
- Alignment No. 16414
- gi No. 225131
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2694: from 4 to 23
- Alignment No. 16415
- gi No. 225144
- % Identity 71.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2694: from 3 to 23
- Alignment No. 16416
- gi No. 225146
- % Identity 70
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2694: from 4 to 23
- Alignment No. 16417
- gi No. 2407285
- % Identity 70.3
- Alignment Length 37
- Location of Alignment in SEQ ID NO 2694: from 1 to 37
- Alignment No. 16418
- gi No. 2497897
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2694: from 1 to 48
- Alignment No. 16419
- gi No. 2497903
- % Identity 76.9
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2694: from 1 to 52
- Alignment No. 16420



- gi No. 2662415
- % Identity 72.5
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2694: from 2 to 52
  
- Alignment No. 16421
- gi No. 2815246
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2694: from 1 to 47
  
- Alignment No. 16422
- gi No. 541943
- % Identity 75
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2694: from 1 to 48

Maximum Length Sequence corresponding to clone ID 317283

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2695
- Ceres seq\_id 1504277

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2696
- Ceres seq\_id 1504278
- Location of start within SEQ ID NO 2695: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16423
- gi No. 2145062
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2696: from 70 to 80

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2697
- Ceres seq\_id 1504279
- Location of start within SEQ ID NO 2695: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16424
- Collagen triple helix repeat (20 copies)
- Location within SEQ ID NO 2697: from 7 to 57 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16425
- gi No. 1042189
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16426
- gi No. 1042189
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16427
- gi No. 131036

- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16428
- gi No. 131036
- % Identity 83.3
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16429
- gi No. 1703594
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 3 to 13
  
- Alignment No. 16430
- gi No. 2134213
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2697: from 27 to 37
  
- Alignment No. 16431
- gi No. 2134213
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16432
- gi No. 2134213
- % Identity 78.6
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2697: from 25 to 38
  
- Alignment No. 16433
- gi No. 2498095
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16434
- gi No. 462338
- % Identity 75
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2697: from 27 to 38
  
- Alignment No. 16435
- gi No. 462338
- % Identity 76.9
- Alignment Length 13
- Location of Alignment in SEQ ID NO 2697: from 27 to 38

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2698
- Ceres seq\_id 1504280
- Location of start within SEQ ID NO 2695: at 119 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- (D) Related Amino Acid Sequences
- Alignment No. 16436

- gi No. 2145062
- % Identity 72.7
- Alignment Length 11
- Location of Alignment in SEQ ID NO 2698: from 31 to 41

Maximum Length Sequence corresponding to clone ID 317408

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2699
- Ceres seq\_id 1504299

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2700
- Ceres seq\_id 1504300
- Location of start within SEQ ID NO 2699: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16437
- Chitin recognition protein
- Location within SEQ ID NO 2700: from 42 to 76 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16438
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2700: from 26 to 76
- Alignment No. 16439
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2700: from 26 to 76

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2701
- Ceres seq\_id 1504301
- Location of start within SEQ ID NO 2699: at 34 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16440
- Chitin recognition protein
- Location within SEQ ID NO 2701: from 31 to 65 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16441
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2701: from 15 to 65
- Alignment No. 16442
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2701: from 15 to 65

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2702
- Ceres seq\_id 1504302
- Location of start within SEQ ID NO 2699: at 40 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16443
- Chitin recognition protein
- Location within SEQ ID NO 2702: from 29 to 63 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16444
- gi No. 116329
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2702: from 13 to 63
- Alignment No. 16445
- gi No. 283037
- % Identity 71.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2702: from 13 to 63

Maximum Length Sequence corresponding to clone ID 317416

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2703
- Ceres seq\_id 1504303

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2704
- Ceres seq\_id 1504304
- Location of start within SEQ ID NO 2703: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16446
- PCI domain
- Location within SEQ ID NO 2704: from 99 to 149 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2705
- Ceres seq\_id 1504305
- Location of start within SEQ ID NO 2703: at 106 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16447
- PCI domain
- Location within SEQ ID NO 2705: from 64 to 114 aa.

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2706
- Ceres seq\_id 1504306
- Location of start within SEQ ID NO 2703: at 196 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16448
- PCI domain
- Location within SEQ ID NO 2706: from 34 to 84 aa.

(D) Related Amino Acid Sequences

Maximum Length Sequence corresponding to clone ID 317417

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2707
- Ceres seq\_id 1504307

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2708
- Ceres seq\_id 1504308
- Location of start within SEQ ID NO 2707: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2709
- Ceres seq\_id 1504309
- Location of start within SEQ ID NO 2707: at 83 nt.

(C) Nomination and Annotation of Domains within Predicted  
Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16449
- gi No. 133902
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16450
- gi No. 1350971
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16451
- gi No. 1350972
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16452
- gi No. 2078466
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
- Alignment No. 16453
- gi No. 2500501
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16454
- gi No. 2979561
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
- Alignment No. 16455
- gi No. 3098456

- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2709: from 11 to 54
  
- Alignment No. 16456
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
  
- Alignment No. 16457
- gi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2709: from 1 to 54
  
- Alignment No. 16458
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2709: from 7 to 54
  
- Alignment No. 16459
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54
  
- Alignment No. 16460
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2709: from 8 to 54

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2710
- Ceres seq\_id 1504310
- Location of start within SEQ ID NO 2707: at 185 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16461
- gi No. 133902
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16462
- gi No. 1350971
- % Identity 88.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16463
- gi No. 1350972
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20
  
- Alignment No. 16464

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- gi No. 2078466
- % Identity 74.5
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16465
- gi No. 2500501
- % Identity 96.3
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16466
- gi No. 2979561
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16467
- gi No. 3098456
- % Identity 72.7
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16468
- gi No. 4038471
- % Identity 98.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16469
- gi No. 4193382
- % Identity 92.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16470
- gi No. 4321094
- % Identity 70.8
- Alignment Length 48
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16471
- gi No. 4432748
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

- Alignment No. 16472
- gi No. 4506711
- % Identity 76.6
- Alignment Length 47
- Location of Alignment in SEQ ID NO 2710: from 1 to 20

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Maximum Length Sequence corresponding to clone ID 317418

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2711
- Ceres seq id 1504311

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2712
- Ceres seq\_id 1504312
- Location of start within SEQ ID NO 2711: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2713
- Ceres seq\_id 1504313
- Location of start within SEQ ID NO 2711: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16473
- gi No. 100789
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16474
- gi No. 100883
- % Identity 93.2
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16475
- gi No. 1122313
- % Identity 79.5
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16476
- gi No. 1122315
- % Identity 75
- Alignment Length 44
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16477
- gi No. 123541
- % Identity 77.8
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22
- Alignment No. 16478
- gi No. 123545
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16479
- gi No. 123546
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22
- Alignment No. 16480
- gi No. 1536911
- % Identity 75
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43



- Alignment No. 16481
- gi No. 232272
- % Identity 70.6
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21
- Alignment No. 16482
- gi No. 445136
- % Identity 70.5
- Alignment Length 45
- Location of Alignment in SEQ ID NO 2713: from 1 to 43
- Alignment No. 16483
- gi No. 507209
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2713: from 5 to 21
- Alignment No. 16484
- gi No. 81638
- % Identity 72.2
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2713: from 5 to 22

Maximum Length Sequence corresponding to clone ID 317460

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2714
- Ceres seq\_id 1504333

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2715
- Ceres seq\_id 1504334
- Location of start within SEQ ID NO 2714: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16485
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2715: from 1 to 99
- Alignment No. 16486
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2715: from 1 to 83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2716
- Ceres seq\_id 1504335
- Location of start within SEQ ID NO 2714: at 20 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16487
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2716: from 1 to 93

- Alignment No. 16488
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2716: from 1 to 77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2717
- Ceres seq\_id 1504336
- Location of start within SEQ ID NO 2714: at 107 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16489
- gi No. 4469020
- % Identity 88.9
- Alignment Length 99
- Location of Alignment in SEQ ID NO 2717: from 1 to 64
- Alignment No. 16490
- gi No. 4680205
- % Identity 98.8
- Alignment Length 83
- Location of Alignment in SEQ ID NO 2717: from 1 to 48

Maximum Length Sequence corresponding to clone ID 317528

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2718
- Ceres seq\_id 1504370

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2719
- Ceres seq\_id 1504371
- Location of start within SEQ ID NO 2718: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2720
- Ceres seq\_id 1504372
- Location of start within SEQ ID NO 2718: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16491
- gi No. 2997589
- % Identity 87.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2720: from 1 to 116
- Alignment No. 16492
- gi No. 2997591
- % Identity 84.6
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
- Alignment No. 16493

- gi No. 2997593
- % Identity 86.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117
- Alignment No. 16494
- gi No. 3319374
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2720: from 93 to 116
- Alignment No. 16495
- gi No. 3367515
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2720: from 1 to 117

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2721
- Ceres seq\_id 1504373
- Location of start within SEQ ID NO 2718: at 23 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16496
- gi No. 2997589
- % Identity 87.1
- Alignment Length 116
- Location of Alignment in SEQ ID NO 2721: from 1 to 109
- Alignment No. 16497
- gi No. 2997591
- % Identity 84.6
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110
- Alignment No. 16498
- gi No. 2997593
- % Identity 86.3
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110
- Alignment No. 16499
- gi No. 3319374
- % Identity 79.2
- Alignment Length 24
- Location of Alignment in SEQ ID NO 2721: from 86 to 109
- Alignment No. 16500
- gi No. 3367515
- % Identity 82.9
- Alignment Length 117
- Location of Alignment in SEQ ID NO 2721: from 1 to 110

Maximum Length Sequence corresponding to clone ID 317547

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2722
- Ceres seq\_id 1504374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2723

- Ceres seq\_id 1504375
- Location of start within SEQ ID NO 2722: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16501
- E1-E2 ATPases
- Location within SEQ ID NO 2723: from 2 to 149 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16502
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149
- Alignment No. 16503
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149
- Alignment No. 16504
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2723: from 2 to 149

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2724
- Ceres seq\_id 1504376
- Location of start within SEQ ID NO 2722: at 12 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16505
- E1-E2 ATPases
- Location within SEQ ID NO 2724: from 1 to 146 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16506
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146
- Alignment No. 16507
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146
- Alignment No. 16508
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2724: from 1 to 146

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2725
- Ceres seq\_id 1504377

- Location of start within SEQ ID NO 2722: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 16509
- E1-E2 ATPases
- Location within SEQ ID NO 2725: from 1 to 136 aa.

(D) Related Amino Acid Sequences

- Alignment No. 16510
- gi No. 2668492
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136
- Alignment No. 16511
- gi No. 3549654
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136
- Alignment No. 16512
- gi No. 4490319
- % Identity 77.7
- Alignment Length 148
- Location of Alignment in SEQ ID NO 2725: from 1 to 136

Maximum Length Sequence corresponding to clone ID 317650

(A) Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 2726
- Ceres seq\_id 1504382

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2727
- Ceres seq\_id 1504383
- Location of start within SEQ ID NO 2726: at 2 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(D) Related Amino Acid Sequences

- Alignment No. 16513
- gi No. 100490
- % Identity 91.7
- Alignment Length 12
- Location of Alignment in SEQ ID NO 2727: from 36 to 47
- Alignment No. 16514
- gi No. 100490
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16515
- gi No. 100490
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16516
- gi No. 100490
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16517
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16518
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16519
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16520
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16521
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16522
- gi No. 100524
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16523
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16524
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16525
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16526
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16527
- gi No. 100525
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16528
- gi No. 100598
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16529
- gi No. 100599
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16530
- gi No. 100812
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16531
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16532
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16533
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16534
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16535
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16536
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16537
- gi No. 100934
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16538
- gi No. 102062
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16539
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16540
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16541
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16542
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16543
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16544
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16545
- gi No. 102278
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16546
- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16547



- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16548
- gi No. 102279
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16549
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16550
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16551
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16552
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16553
- gi No. 102280
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16554
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16555
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16556
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16557
- gi No. 102281

- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16558
- gi No. 102281
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16559
- gi No. 102389
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16560
- gi No. 103436
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16561
- gi No. 1044940
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16562
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16563
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16564
- gi No. 104829
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16565
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16566
- gi No. 1050930
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16567
- gi No. 10673
- % Identity 81

- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16568  
- gi No. 1070590  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16569  
- gi No. 1070590  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16570  
- gi No. 1070590  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16571  
- gi No. 1070591  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16572  
- gi No. 1070591  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16573  
- gi No. 1070591  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16574  
- gi No. 1070591  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16575  
- gi No. 1070591  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16576  
- gi No. 1070591  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16577  
- gi No. 1070591  
- % Identity 85.7  
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16578
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16579
- gi No. 1070591
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16580
- gi No. 1076678
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16581
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16582
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16583
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16584
- gi No. 1076708
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16585
- gi No. 1078777
- % Identity 70.4
- Alignment Length 27
- Location of Alignment in SEQ ID NO 2727: from 27 to 51
- Alignment No. 16586
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16587
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16588
- gi No. 1078813
- % Identity 71.4
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16589
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16590
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16591
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16592
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16593
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16594
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16595
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16596
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16597
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16598
- gi No. 1083758
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16599
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16600
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16601
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16602
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16603
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16604
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16605
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16606
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16607
- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16608

- gi No. 1101011
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16609
- gi No. 1101013
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 16610
- gi No. 1101015
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 16611
- gi No. 1101021
- % Identity 73.3
- Alignment Length 15
- Location of Alignment in SEQ ID NO 2727: from 33 to 47
  
- Alignment No. 16612
- gi No. 1101021
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16613
- gi No. 1107481
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 16614
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16615
- gi No. 1107481
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16616
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16617
- gi No. 1143188
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16618
- gi No. 1143188

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16619
- gi No. 1167510
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 16620
- gi No. 1167510
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16621
- gi No. 1174859
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16622
- gi No. 1174860
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16623
- gi No. 1174861
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16624
- gi No. 1184755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16625
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16626
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16627
- gi No. 1197093
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16628
- gi No. 1197093
- % Identity 85.7



- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16629
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16630
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16631
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16632
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16633
- gi No. 1304128
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16634
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16635
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16636
- gi No. 1304128
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16637
- gi No. 1304357
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16638
- gi No. 1321735
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16639
  - gi No. 1321735
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16640
  - gi No. 1326022
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16641
  - gi No. 1326022
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16642
  - gi No. 1332579
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16643
  - gi No. 1332579
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16644
  - gi No. 1332579
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16645
  - gi No. 1332579
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16646
  - gi No. 1332579
  - % Identity 81
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16647
  - gi No. 1332579
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16648
  - gi No. 1332579
  - % Identity 85.7
  - Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16649
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16650
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16651
- gi No. 1332579
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16652
- gi No. 1351348
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16653
- gi No. 1351349
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16654
- gi No. 1353755
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16655
- gi No. 1353757
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 28 to 47
  
- Alignment No. 16656
- gi No. 1353757
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16657
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16658
- gi No. 1362008
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16659
- gi No. 1362008
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16660
- gi No. 1362008
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16661
- gi No. 1362009
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16662
- gi No. 1362010
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16663
- gi No. 1362010
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16664
- gi No. 1362010
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16665
- gi No. 1362012
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16666
- gi No. 1362012
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16667
- gi No. 136665
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16668
- gi No. 136666
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16669

- gi No. 136667  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16670  
- gi No. 136668  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16671  
- gi No. 136669  
- % Identity 71.4  
- Alignment Length 28  
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16672  
- gi No. 136670  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16673  
- gi No. 136671  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16674  
- gi No. 136672  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16675  
- gi No. 136673  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16676  
- gi No. 136674  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16677  
- gi No. 136675  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16678  
- gi No. 136676  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16679  
- gi No. 136677

- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16680
- gi No. 136678
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16681
- gi No. 1421797
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16682
- gi No. 156480
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16683
- gi No. 158759
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16684
- gi No. 158763
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16685
- gi No. 158765
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16686
- gi No. 158767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16687
- gi No. 158769
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16688
- gi No. 158771
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16689
- gi No. 161281
- % Identity 85.7

- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16690
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16691
- gi No. 163575
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16692
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16693
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16694
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16695
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16696
- gi No. 166336
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16697
- gi No. 166336
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16698
- gi No. 1666175
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16699
- gi No. 1675359
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16700  
- gi No. 167935  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16701  
- gi No. 167935  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16702  
- gi No. 167935  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16703  
- gi No. 167935  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16704  
- gi No. 167935  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16705  
- gi No. 167941  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 28 to 48

- Alignment No. 16706  
- gi No. 167945  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16707  
- gi No. 167945  
- % Identity 81.8  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16708  
- gi No. 167945  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16709  
- gi No. 167947  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48



- Alignment No. 16710  
- gi No. 167947  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16711  
- gi No. 167947  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16712  
- gi No. 167947  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16713  
- gi No. 167947  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16714  
- gi No. 167947  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16715  
- gi No. 167947  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16716  
- gi No. 167949  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16717  
- gi No. 167949  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16718  
- gi No. 167949  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16719  
- gi No. 167949  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16720
- gi No. 167949
- % Identity 86.4
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 16721
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16722
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16723
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16724
- gi No. 1684855
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16725
- gi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16726
- gi No. 1684857
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16727
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16728
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16729
- gi No. 170352
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16730

- gi No. 170352  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16731  
- gi No. 170352  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16732  
- gi No. 170352  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16733  
- gi No. 170354  
- % Identity 88.2  
- Alignment Length 17  
- Location of Alignment in SEQ ID NO 2727: from 31 to 47

- Alignment No. 16734  
- gi No. 170354  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16735  
- gi No. 170354  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16736  
- gi No. 170354  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16737  
- gi No. 170354  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16738  
- gi No. 1762374  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16739  
- gi No. 1762935  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16740  
- gi No. 1763015

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16741
- gi No. 1771780
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16742
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16743
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16744
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16745
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16746
- gi No. 1778712
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16747
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16748
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16749
- gi No. 1800281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16750
- gi No. 1800281
- % Identity 85.7

- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16751  
- gi No. 1800281  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16752  
- gi No. 1805696  
- % Identity 85.7  
- Alignment Length 14  
- Location of Alignment in SEQ ID NO 2727: from 34 to 47

- Alignment No. 16753  
- gi No. 1805696  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16754  
- gi No. 1839584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16755  
- gi No. 1841849  
- % Identity 87.5  
- Alignment Length 16  
- Location of Alignment in SEQ ID NO 2727: from 27 to 42

- Alignment No. 16756  
- gi No. 208558  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16757  
- gi No. 208560  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16758  
- gi No. 208562  
- % Identity 76.2  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16759  
- gi No. 208564  
- % Identity 76.2  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16760  
- gi No. 208566  
- % Identity 81  
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16761
- gi No. 208568
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16762
- gi No. 208891
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16763
- gi No. 208891
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16764
- gi No. 209603
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16765
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16766
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16767
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16768
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16769
- gi No. 2118958
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16770
- gi No. 2118959
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16771  
- gi No. 2118959  
- % Identity 77.3  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16772  
- gi No. 2118959  
- % Identity 72.7  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 16773  
- gi No. 2118960  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16774  
- gi No. 2118960  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16775  
- gi No. 2118961  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16776  
- gi No. 2118961  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16777  
- gi No. 2118962  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16778  
- gi No. 2118962  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16779  
- gi No. 2118964  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16780  
- gi No. 2118964  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16781
- gi No. 2118964
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16782
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16783
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16784
- gi No. 2118965
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16785
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16786
- gi No. 2129452
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16787
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16788
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16789
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16790
- gi No. 2129452
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16791



- gi No. 2133278  
- % Identity 75  
- Alignment Length 28  
- Location of Alignment in SEQ ID NO 2727: from 27 to 52

- Alignment No. 16792  
- gi No. 2133549  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16793  
- gi No. 2144011  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16794  
- gi No. 2144275  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16795  
- gi No. 2144734  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16796  
- gi No. 2144734  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16797  
- gi No. 2144734  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16798  
- gi No. 2144734  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16799  
- gi No. 2149467  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16800  
- gi No. 2209091  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16801  
- gi No. 2209091

- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16802
- gi No. 223061
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16803
- gi No. 224321
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16804
- gi No. 224321
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16805
- gi No. 225317
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16806
- gi No. 225319
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16807
- gi No. 225320
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16808
- gi No. 2281952
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
  
- Alignment No. 16809
- gi No. 2281954
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
  
- Alignment No. 16810
- gi No. 2281955
- % Identity 85.7
- Alignment Length 14
- Location of Alignment in SEQ ID NO 2727: from 34 to 47
  
- Alignment No. 16811
- gi No. 2281959
- % Identity 73.3

- Alignment Length 15  
- Location of Alignment in SEQ ID NO 2727: from 33 to 47

- Alignment No. 16812  
- gi No. 2330875  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16813  
- gi No. 2408009  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16814  
- gi No. 2437825  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16815  
- gi No. 2437825  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16816  
- gi No. 2437825  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16817  
- gi No. 2437825  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16818  
- gi No. 247308  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16819  
- gi No. 248865  
- % Identity 80  
- Alignment Length 20  
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 16820  
- gi No. 2558539  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16821  
- gi No. 2627129  
- % Identity 85.7  
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16822
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16823
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16824
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16825
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16826
- gi No. 2627129
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16827
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16828
- gi No. 2627129
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16829
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16830
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16831
- gi No. 2627131
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16832  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16833  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16834  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16835  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16836  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16837  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16838  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16839  
- gi No. 2627131  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16840  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16841  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16842  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16843  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16844  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16845  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16846  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16847  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16848  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16849  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16850  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16851  
- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16852

- gi No. 2627133  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16853  
- gi No. 2641213  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16854  
- gi No. 2641213  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16855  
- gi No. 2654141  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16856  
- gi No. 2654141  
- % Identity 76.2  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16857  
- gi No. 2654141  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16858  
- gi No. 2654141  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16859  
- gi No. 2654141  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16860  
- gi No. 2707837  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16861  
- gi No. 2707837  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16862  
- gi No. 2707837

- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16863  
- gi No. 2707837  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16864  
- gi No. 2739333  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16865  
- gi No. 2739333  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16866  
- gi No. 2739333  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16867  
- gi No. 2739333  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16868  
- gi No. 2760345  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16869  
- gi No. 2760345  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16870  
- gi No. 2760345  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16871  
- gi No. 2760345  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16872  
- gi No. 2760347  
- % Identity 85.7



- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16873
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16874
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16875
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16876
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16877
- gi No. 2760347
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16878
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16879
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16880
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16881
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16882
- gi No. 2760349
- % Identity 85.7
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16883
- gi No. 279635
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16884
- gi No. 279636
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16885
- gi No. 280386
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16886
- gi No. 281276
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 16887
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16888
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16889
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16890
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16891
- gi No. 283496
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16892
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16893
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16894
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16895
- gi No. 2894304
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16896
- gi No. 2894306
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16897
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16898
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16899
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16900
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16901
- gi No. 2894308
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 16902
- gi No. 2995949
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16903
  - gi No. 3047314
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16904
  - gi No. 3047316
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16905
  - gi No. 3047318
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16906
  - gi No. 3047318
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16907
  - gi No. 3047318
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16908
  - gi No. 3047318
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16909
  - gi No. 3047318
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16910
  - gi No. 3091264
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16911
  - gi No. 3091264
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16912
  - gi No. 3091264
  - % Identity 85.7
  - Alignment Length 21
  - Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16913

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- gi No. 3091264
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16914
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16915
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16916
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16917
- gi No. 3126967
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16918
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16919
- gi No. 3126967
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16920
- gi No. 3152950
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16921
- gi No. 3158372
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16922
- gi No. 3158372
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16923
- gi No. 320608

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- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16924  
- gi No. 320608  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16925  
- gi No. 320608  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16926  
- gi No. 320608  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16927  
- gi No. 322750  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16928  
- gi No. 323071  
- % Identity 76.2  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16929  
- gi No. 323157  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16930  
- gi No. 323157  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16931  
- gi No. 323157  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16932  
- gi No. 323157  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16933  
- gi No. 323157  
- % Identity 85.7

- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16934  
- gi No. 323157  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16935  
- gi No. 323208  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16936  
- gi No. 323230  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16937  
- gi No. 3265058  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16938  
- gi No. 3319208  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16939  
- gi No. 3335355  
- % Identity 85  
- Alignment Length 20  
- Location of Alignment in SEQ ID NO 2727: from 27 to 46

- Alignment No. 16940  
- gi No. 3335355  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16941  
- gi No. 3335355  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16942  
- gi No. 3335355  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16943  
- gi No. 340062  
- % Identity 88.2  
- Alignment Length 17

- Location of Alignment in SEQ ID NO 2727: from 31 to 47
- Alignment No. 16944
- gi No. 3452083
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16945
- gi No. 348148
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16946
- gi No. 3603456
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16947
- gi No. 3603456
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16948
- gi No. 3603456
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 16949
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16950
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16951
- gi No. 3687425
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16952
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16953
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47



- Alignment No. 16954
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16955
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16956
- gi No. 3738185
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16957
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16958
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16959
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16960
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16961
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16962
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16963
- gi No. 3776536
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16964  
- gi No. 3776536  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16965  
- gi No. 3789940  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16966  
- gi No. 3789940  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16967  
- gi No. 3789940  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16968  
- gi No. 3789940  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16969  
- gi No. 3789942  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16970  
- gi No. 3789942  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16971  
- gi No. 3789942  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16972  
- gi No. 3789942  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16973  
- gi No. 3789942  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16974

- gi No. 385076  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16975  
- gi No. 3882081  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16976  
- gi No. 3882081  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16977  
- gi No. 3882081  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16978  
- gi No. 3885463  
- % Identity 83.3  
- Alignment Length 18  
- Location of Alignment in SEQ ID NO 2727: from 30 to 47

- Alignment No. 16979  
- gi No. 3892189  
- % Identity 70.4  
- Alignment Length 27  
- Location of Alignment in SEQ ID NO 2727: from 27 to 51

- Alignment No. 16980  
- gi No. 402242  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16981  
- gi No. 4105408  
- % Identity 91.7  
- Alignment Length 12  
- Location of Alignment in SEQ ID NO 2727: from 36 to 47

- Alignment No. 16982  
- gi No. 4105408  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16983  
- gi No. 4105408  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16984  
- gi No. 4105408

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16985
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16986
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16987
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16988
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16989
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16990
- gi No. 4115337
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16991
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16992
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16993
- gi No. 4150898
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 16994
- gi No. 4150898
- % Identity 85.7

- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16995  
- gi No. 4150912  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16996  
- gi No. 4150912  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16997  
- gi No. 4150912  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16998  
- gi No. 4150912  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 16999  
- gi No. 4150912  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17000  
- gi No. 4150914  
- % Identity 86.7  
- Alignment Length 15  
- Location of Alignment in SEQ ID NO 2727: from 33 to 47

- Alignment No. 17001  
- gi No. 4150914  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17002  
- gi No. 4151082  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17003  
- gi No. 418854  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17004  
- gi No. 418854  
- % Identity 85.7  
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17005
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17006
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17007
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17008
- gi No. 418854
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17009
- gi No. 421735
- % Identity 88.9
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17010
- gi No. 421867
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17011
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17012
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17013
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17014
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17015
- gi No. 421929
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17016
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17017
- gi No. 421929
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17018
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17019
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17020
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17021
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17022
- gi No. 422248
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17023
- gi No. 422269
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17024
- gi No. 422270
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17025
- gi No. 422271
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17026
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17027
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17028
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17029
- gi No. 433970
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17030
- gi No. 433970
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17031
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17032
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17033
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17034
- gi No. 444791
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17035



- gi No. 4506713  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17036  
- gi No. 4507761  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17037  
- gi No. 456779  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17038  
- gi No. 4586594  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17039  
- gi No. 4586594  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17040  
- gi No. 4587232  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17041  
- gi No. 4587234  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17042  
- gi No. 4587236  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17043  
- gi No. 4587236  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17044  
- gi No. 4587236  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17045  
- gi No. 4587236

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17046
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17047
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17048
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17049
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17050
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17051
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17052
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17053
- gi No. 4587236
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17054
- gi No. 4589760
- % Identity 75
- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
  
- Alignment No. 17055
- gi No. 4589760
- % Identity 75

- Alignment Length 28
- Location of Alignment in SEQ ID NO 2727: from 27 to 52
- Alignment No. 17056
- gi No. 463363
- % Identity 70
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 17057
- gi No. 463369
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17058
- gi No. 463373
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17059
- gi No. 463375
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17060
- gi No. 464989
- % Identity 71.4
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17061
- gi No. 464990
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17062
- gi No. 468272
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17063
- gi No. 4737
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17064
- gi No. 477630
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17065
- gi No. 477815
- % Identity 81
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17066
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17067
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17068
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17069
- gi No. 478811
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17070
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17071
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17072
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17073
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17074
- gi No. 4809266
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17075
- gi No. 481477
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17076  
- gi No. 481477  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17077  
- gi No. 481477  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17078  
- gi No. 481477  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17079  
- gi No. 481477  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17080  
- gi No. 481477  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17081  
- gi No. 485427  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17082  
- gi No. 485518  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17083  
- gi No. 49586  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17084  
- gi No. 49586  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17085  
- gi No. 49586  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17086
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17087
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17088
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17089
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17090
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17091
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17092
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17093
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17094
- gi No. 510473
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17095
- gi No. 510476
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17096

- gi No. 5107695  
- % Identity 76.2  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17097  
- gi No. 539404  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17098  
- gi No. 539935  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17099  
- gi No. 539935  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17100  
- gi No. 539935  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17101  
- gi No. 539935  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17102  
- gi No. 541546  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17103  
- gi No. 541546  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17104  
- gi No. 541546  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17105  
- gi No. 541546  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17106  
- gi No. 541546

- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17107  
- gi No. 541953  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17108  
- gi No. 541954  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17109  
- gi No. 5441519  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17110  
- gi No. 552237  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17111  
- gi No. 5523967  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17112  
- gi No. 5523969  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17113  
- gi No. 5523969  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17114  
- gi No. 5523971  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17115  
- gi No. 5523973  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17116  
- gi No. 5523975  
- % Identity 85.7



- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17117  
- gi No. 5523977  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17118  
- gi No. 5523979  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17119  
- gi No. 5523979  
- % Identity 72.4  
- Alignment Length 29  
- Location of Alignment in SEQ ID NO 2727: from 19 to 47

- Alignment No. 17120  
- gi No. 5523981  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17121  
- gi No. 5523985  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17122  
- gi No. 5523987  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17123  
- gi No. 5531273  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17124  
- gi No. 5531273  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17125  
- gi No. 5531273  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17126  
- gi No. 5531273  
- % Identity 85.7  
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17127
- gi No. 5531273
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17128
- gi No. 5531278
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17129
- gi No. 5531281
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17130
- gi No. 554564
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17131
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17132
- gi No. 567767
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17133
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17134
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17135
- gi No. 571519
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17136
- gi No. 571519
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17137  
- gi No. 571519  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17138  
- gi No. 571519  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17139  
- gi No. 576773  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17140  
- gi No. 576773  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17141  
- gi No. 576773  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17142  
- gi No. 576773  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17143  
- gi No. 576773  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17144  
- gi No. 576775  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17145  
- gi No. 578545  
- % Identity 77.3  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17146  
- gi No. 578545  
- % Identity 72.7  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17147
- gi No. 578546
- % Identity 81.8
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17148
- gi No. 578546
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17149
- gi No. 578546
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17150
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17151
- gi No. 578549
- % Identity 72.7
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17152
- gi No. 578551
- % Identity 73.7
- Alignment Length 19
- Location of Alignment in SEQ ID NO 2727: from 29 to 47
  
- Alignment No. 17153
- gi No. 578551
- % Identity 77.3
- Alignment Length 22
- Location of Alignment in SEQ ID NO 2727: from 27 to 48
  
- Alignment No. 17154
- gi No. 600539
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17155
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17156
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17157

- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17158
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17159
- gi No. 602076
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17160
- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17161
- gi No. 625174
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17162
- gi No. 625509
- % Identity 85
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
  
- Alignment No. 17163
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17164
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17165
- gi No. 625509
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17166
- gi No. 630455
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17167
- gi No. 630479

- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17168  
- gi No. 630479  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17169  
- gi No. 630479  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17170  
- gi No. 630479  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17171  
- gi No. 630479  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17172  
- gi No. 630479  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17173  
- gi No. 70636  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17174  
- gi No. 70636  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17175  
- gi No. 70636  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17176  
- gi No. 70637  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17177  
- gi No. 70639  
- % Identity 85.7

- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17178  
- gi No. 70639  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17179  
- gi No. 70639  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17180  
- gi No. 70639  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17181  
- gi No. 70640  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17182  
- gi No. 70642  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17183  
- gi No. 70642  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17184  
- gi No. 70642  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17185  
- gi No. 70642  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17186  
- gi No. 70642  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17187  
- gi No. 70643  
- % Identity 85.7  
- Alignment Length 21

- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17188
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17189
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17190
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17191
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17192
- gi No. 70644
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17193
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17194
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17195
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17196
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17197
- gi No. 70645
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17198  
- gi No. 70646  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17199  
- gi No. 70647  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17200  
- gi No. 70647  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17201  
- gi No. 70647  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17202  
- gi No. 70648  
- % Identity 81  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17203  
- gi No. 70650  
- % Identity 72.2  
- Alignment Length 18  
- Location of Alignment in SEQ ID NO 2727: from 27 to 44

- Alignment No. 17204  
- gi No. 70653  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17205  
- gi No. 70654  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17206  
- gi No. 70657  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17207  
- gi No. 70658  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17208  
- gi No. 70659  
- % Identity 87.5  
- Alignment Length 16  
- Location of Alignment in SEQ ID NO 2727: from 32 to 47

- Alignment No. 17209  
- gi No. 70660  
- % Identity 81.8  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17210  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17211  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17212  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17213  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17214  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17215  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17216  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17217  
- gi No. 726391  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17218

- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17219
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17220
- gi No. 726391
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17221
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17222
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17223
- gi No. 82040
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17224
- gi No. 82040
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17225
- gi No. 82284
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17226
- gi No. 82287
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17227
- gi No. 82426
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17228
- gi No. 82426

- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17229  
- gi No. 82512  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17230  
- gi No. 82512  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17231  
- gi No. 82733  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17232  
- gi No. 82734  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17233  
- gi No. 82734  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17234  
- gi No. 82734  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17235  
- gi No. 83594  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17236  
- gi No. 83596  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17237  
- gi No. 83596  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17238  
- gi No. 83596  
- % Identity 85.7

- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17239  
- gi No. 83596  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17240  
- gi No. 83596  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17241  
- gi No. 84151  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17242  
- gi No. 84151  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17243  
- gi No. 84151  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17244  
- gi No. 84152  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17245  
- gi No. 84152  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17246  
- gi No. 84152  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17247  
- gi No. 84152  
- % Identity 86.4  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2727: from 27 to 48

- Alignment No. 17248  
- gi No. 84152  
- % Identity 86.4  
- Alignment Length 22

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Location of Alignment in SEQ ID NO 2727: from 27 to 48
- Alignment No. 17249
- gi No. 84337
- % Identity 83.3
- Alignment Length 18
- Location of Alignment in SEQ ID NO 2727: from 27 to 44
- Alignment No. 17250
- gi No. 84337
- % Identity 81
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17251
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17252
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17253
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17254
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17255
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17256
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17257
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17258
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

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- Alignment No. 17259
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17260
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17261
- gi No. 84478
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17262
- gi No. 84834
- % Identity 87.5
- Alignment Length 16
- Location of Alignment in SEQ ID NO 2727: from 27 to 42
  
- Alignment No. 17263
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17264
- gi No. 84834
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17265
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17266
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17267
- gi No. 85106
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17268
- gi No. 870794
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17269
- gi No. 870794
- % Identity 76.2
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17270
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17271
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17272
- gi No. 89311
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17273
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17274
- gi No. 899115
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17275
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17276
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17277
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17278
- gi No. 899608
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
  
- Alignment No. 17279



- gi No. 899608  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17280  
- gi No. 902525  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17281  
- gi No. 902584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17282  
- gi No. 902584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17283  
- gi No. 902584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17284  
- gi No. 902584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17285  
- gi No. 902584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17286  
- gi No. 902584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17287  
- gi No. 902584  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17288  
- gi No. 902586  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17289  
- gi No. 902586

- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17290
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17291
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17292
- gi No. 902586
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17293
- gi No. 91870
- % Identity 80
- Alignment Length 20
- Location of Alignment in SEQ ID NO 2727: from 27 to 46
- Alignment No. 17294
- gi No. 91870
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17295
- gi No. 91871
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17296
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17297
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17298
- gi No. 940395
- % Identity 85.7
- Alignment Length 21
- Location of Alignment in SEQ ID NO 2727: from 27 to 47
- Alignment No. 17299
- gi No. 940395
- % Identity 85.7

- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17300  
- gi No. 940395  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17301  
- gi No. 940395  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17302  
- gi No. 940395  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17303  
- gi No. 940395  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17304  
- gi No. 967985  
- % Identity 88.9  
- Alignment Length 18  
- Location of Alignment in SEQ ID NO 2727: from 27 to 44

- Alignment No. 17305  
- gi No. 99771  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17306  
- gi No. 99772  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

- Alignment No. 17307  
- gi No. 99975  
- % Identity 85.7  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2727: from 27 to 47

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2728  
- Ceres seq\_id 1504384  
- Location of start within SEQ ID NO 2726: at 166 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Alignment No. 17308  
- Ubiquitin family  
- Location within SEQ ID NO 2728: from 1 to 49 aa.

(D) Related Amino Acid Sequences

- Alignment No. 17309
  - gi No. 100490
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17310
  - gi No. 100490
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17311
  - gi No. 100490
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17312
  - gi No. 100490
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17313
  - gi No. 100524
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17314
  - gi No. 100524
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17315
  - gi No. 100524
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17316
  - gi No. 100524
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17317
  - gi No. 100524
  - % Identity 81.1
  - Alignment Length 53
  - Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17318
  - gi No. 100524
  - % Identity 79.6
  - Alignment Length 54
  - Location of Alignment in SEQ ID NO 2728: from 1 to 50

- Alignment No. 17319
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17320
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17321
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17322
- gi No. 100525
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17323
- gi No. 100598
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17324
- gi No. 100599
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17325
- gi No. 100812
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17326
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17327
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17328
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17329
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17330
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17331
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17332
- gi No. 100934
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17333
- gi No. 100981
- % Identity 76.7
- Alignment Length 43
- Location of Alignment in SEQ ID NO 2728: from 9 to 51
- Alignment No. 17334
- gi No. 102062
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17335
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17336
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17337
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17338
- gi No. 102278
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17339

- gi No. 102278  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17340  
- gi No. 102278  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17341  
- gi No. 102278  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17342  
- gi No. 102279  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17343  
- gi No. 102279  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17344  
- gi No. 102279  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17345  
- gi No. 102280  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17346  
- gi No. 102280  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17347  
- gi No. 102280  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17348  
- gi No. 102280  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17349  
- gi No. 102280

- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17350
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17351
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17352
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17353
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17354
- gi No. 102281
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17355
- gi No. 102389
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17356
- gi No. 103436
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17357
- gi No. 1044940
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17358
- gi No. 104829
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17359
- gi No. 104829
- % Identity 79.2



- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17360
- gi No. 104829
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17361
- gi No. 1050930
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17362
- gi No. 10673
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17363
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17364
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17365
- gi No. 1070590
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17366
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17367
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17368
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17369
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17370
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17371
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17372
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17373
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17374
- gi No. 1070591
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17375
- gi No. 1076678
- % Identity 78.2
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17376
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17377
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17378
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17379
- gi No. 1076708
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17380
- gi No. 1078777
- % Identity 73.1
- Alignment Length 52
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17381
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17382
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17383
- gi No. 1078813
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17384
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17385
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17386
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17387
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17388
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17389
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17390
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17391
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17392
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17393
- gi No. 1083758
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17394
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17395
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17396
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17397
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17398
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17399
- gi No. 1101011
- % Identity 71.4
- Alignment Length 56
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17400

- gi No. 1101011  
- % Identity 71.4  
- Alignment Length 56  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17401  
- gi No. 1101011  
- % Identity 71.4  
- Alignment Length 56  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17402  
- gi No. 1101011  
- % Identity 71.4  
- Alignment Length 56  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17403  
- gi No. 1101013  
- % Identity 76.2  
- Alignment Length 21  
- Location of Alignment in SEQ ID NO 2728: from 1 to 18

- Alignment No. 17404  
- gi No. 1101021  
- % Identity 71.4  
- Alignment Length 56  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17405  
- gi No. 1101023  
- % Identity 72.5  
- Alignment Length 40  
- Location of Alignment in SEQ ID NO 2728: from 10 to 49

- Alignment No. 17406  
- gi No. 1107481  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17407  
- gi No. 1107481  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17408  
- gi No. 1143188  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17409  
- gi No. 1143188  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17410  
- gi No. 1143188

- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17411
- gi No. 1167510
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17412
- gi No. 1174859
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17413
- gi No. 1174860
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17414
- gi No. 1174861
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17415
- gi No. 1184755
- % Identity 76.4
- Alignment Length 55
- Location of Alignment in SEQ ID NO 2728: from 1 to 51
- Alignment No. 17416
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17417
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17418
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17419
- gi No. 1197093
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17420
- gi No. 1304128
- % Identity 79.2

- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17421
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17422
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17423
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17424
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17425
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17426
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17427
- gi No. 1304128
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17428
- gi No. 1321735
- % Identity 75
- Alignment Length 40
- Location of Alignment in SEQ ID NO 2728: from 1 to 36
- Alignment No. 17429
- gi No. 1321735
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17430
- gi No. 1326021
- % Identity 79.4
- Alignment Length 34

- Location of Alignment in SEQ ID NO 2728: from 16 to 49
- Alignment No. 17431
- gi No. 1326022
- % Identity 76.9
- Alignment Length 39
- Location of Alignment in SEQ ID NO 2728: from 11 to 49
- Alignment No. 17432
- gi No. 1326022
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17433
- gi No. 1326022
- % Identity 74.1
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17434
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17435
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17436
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17437
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17438
- gi No. 1332579
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17439
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17440
- gi No. 1332579
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49



- Alignment No. 17441  
- gi No. 1332579  
- % Identity 81.1  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17442  
- gi No. 1332579  
- % Identity 81.1  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17443  
- gi No. 1332579  
- % Identity 81.1  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17444  
- gi No. 1351348  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17445  
- gi No. 1351349  
- % Identity 75.5  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17446  
- gi No. 1353755  
- % Identity 80.6  
- Alignment Length 36  
- Location of Alignment in SEQ ID NO 2728: from 14 to 49

- Alignment No. 17447  
- gi No. 1353755  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17448  
- gi No. 1353757  
- % Identity 72.7  
- Alignment Length 22  
- Location of Alignment in SEQ ID NO 2728: from 1 to 18

- Alignment No. 17449  
- gi No. 1353757  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17450  
- gi No. 1362008  
- % Identity 81.1  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17451
- gi No. 1362008
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17452
- gi No. 1362008
- % Identity 73.6
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17453
- gi No. 1362008
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17454
- gi No. 1362009
- % Identity 79.6
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17455
- gi No. 1362010
- % Identity 83
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17456
- gi No. 1362010
- % Identity 71.7
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17457
- gi No. 1362010
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17458
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17459
- gi No. 1362012
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17460
- gi No. 136665
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17461

- gi No. 136666  
- % Identity 81.1  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17462  
- gi No. 136667  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17463  
- gi No. 136668  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17464  
- gi No. 136669  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17465  
- gi No. 136670  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17466  
- gi No. 136671  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17467  
- gi No. 136672  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17468  
- gi No. 136673  
- % Identity 81.1  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17469  
- gi No. 136674  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17470  
- gi No. 136675  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17471  
- gi No. 136676

- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17472
- gi No. 136677
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17473
- gi No. 136678
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17474
- gi No. 1421797
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17475
- gi No. 1480012
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17476
- gi No. 158759
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17477
- gi No. 158763
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17478
- gi No. 158765
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17479
- gi No. 158767
- % Identity 75.5
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17480
- gi No. 158769
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17481
- gi No. 158771
- % Identity 77.4

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- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17482  
- gi No. 161281  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17483  
- gi No. 163575  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17484  
- gi No. 163575  
- % Identity 79.2  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17485  
- gi No. 166336  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17486  
- gi No. 166336  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17487  
- gi No. 166336  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17488  
- gi No. 166336  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17489  
- gi No. 166336  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17490  
- gi No. 166336  
- % Identity 77.4  
- Alignment Length 53  
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17491  
- gi No. 1666175  
- % Identity 81.1  
- Alignment Length 53

- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17492
- gi No. 1675359
- % Identity 76.5
- Alignment Length 17
- Location of Alignment in SEQ ID NO 2728: from 1 to 13
- Alignment No. 17493
- gi No. 167935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17494
- gi No. 167935
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17495
- gi No. 167935
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17496
- gi No. 167935
- % Identity 77.4
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17497
- gi No. 167935
- % Identity 75.9
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
- Alignment No. 17498
- gi No. 167941
- % Identity 77.2
- Alignment Length 57
- Location of Alignment in SEQ ID NO 2728: from 1 to 53
- Alignment No. 17499
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17500
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
- Alignment No. 17501
- gi No. 167945
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17502
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17503
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17504
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17505
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17506
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17507
- gi No. 167947
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17508
- gi No. 167947
- % Identity 77.8
- Alignment Length 54
- Location of Alignment in SEQ ID NO 2728: from 1 to 50
  
- Alignment No. 17509
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17510
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17511
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49

- Alignment No. 17512
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17513
- gi No. 167949
- % Identity 79.2
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17514
- gi No. 1684855
- % Identity 81.8
- Alignment Length 33
- Location of Alignment in SEQ ID NO 2728: from 17 to 49
  
- Alignment No. 17515
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17516
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17517
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17518
- gi No. 1684855
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17519
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17520
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17521
- gi No. 1684857
- % Identity 81.1
- Alignment Length 53
- Location of Alignment in SEQ ID NO 2728: from 1 to 49
  
- Alignment No. 17522